### FIGURE 1

R35464	GGC	CGG	GT	CG	TT	CT	CGC	CT	GG	CTG	GGA	::	GC1	CC	TCC	TC	TC!	GG(	GT	CC	50
ORF													(								16
R35464													GAC	TT	CTG	cc	1G0	TG	rcG	AA	100
ORF	W	₽	A	D	5	₹ !	Ē I	2	S	I	Н		D	£	C	L	'	/ :	S	K	33
R35464					λGA	TT	CGG	<b>3</b> G	cc:	rcc.	ATG	cc	TAC	GT	GGI	'GG	TAC	:AA1	rgt	CA	150
ORF	V	٧	G		R	£	R	A	:	5 !	M	P	R	W	W	1	Υ.	N	٧	:	50
R35464	CTG	ACG	GA1	C	CTC	CC/	NGC1	rG	TT	GT	GTA	TG	GGG	GC.	TGT	Ġλ	CGC	i	NCA	GC	200
ORF	D	G	:	5	C	Q	L		F	٧	Y	G	(	3	C	D	G	N	\$	5	55
R35464	AAT	MI	TAC	c	TGA	CCI	MGC	įλ	GGI	AGT	GCC	TC	AAG	ia.	ATG	TG	cci	CT	310	:AC	250
ORF	N I	N	Y	L	1	. 1	< E		3	С	L	)	K	K	C	A	1	,	V	•	8 3
R35464	AGA	:XX	TGC	:c	ACG	GG1	GAC	:c	TGO	CC.	ACC	AG	CAC	GA	ATG	<b>CA</b>	GCC	GA:	TTC	CT	300
ORF	3	N	A		T	G	D	L	1	1	ľ	S	R	N	λ	•	A	D	S	S	100
R35464	CTG1	CC	CAA	G	TGC	TCC	CAC	iλ	AGO	<b>SCA</b> (	GGA	TT	CTI	GA.	AGA	cc	ACT	מדמ	NGC	:GA	350
ORF	V	5	S	;	A	P	R		R	3	D	S	•	٠.	R	P	÷	Ç	P	t	116
R35464	TATO	TT	TCA	A	NTA	TTC	LAN	G	AA1	. 77	TTG	CA	ccc	NC.	AAC	GN	ATT				393
ORF	Y \	' '	S	•	I	•	F	l	I	I	A		5	•	T	•					130

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KEY

R35464 - Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)
ORF - EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

## FIGURE 2

R74593	GCAATAATTA	CCTGACCAAG	GAGGAGTGCC TCAAGAAATG TGCCACTGTC G V P Q E M C H C H	50
ORF	Q L	P D 2 G		17
R74593	ACAGAGAATG	CCACGGGTGA	CCTGGCCACC AGCAGGAATG CAGCGGATTC P G H Q Q E C S G F	100
ORF	R E C	H G *		33
R74593	CTCTGTCCCA	AGTCTCCCAG	AAGGCAGGAT TCTGAAGACC ACTCCAGCGA	150
C F	L C P K	S P R	R Q D S E D H S S D	53
R74593	TATGTTCAAC	TATGAAGAAT	ACTGCACCGC CAACGCAGTC ACTGGGCCTT C T A N A V T G P C	200
ORF	M F N	Y E E Y		67
R74593	GCCGTGCATC	CTTCCCACGC	TGGTACTTTG ACGTGGAGAG GAACTCCTGC W Y F D V E R N S C	250
ORF	R A S	F P R		83
R74593	AATAACTICA	TCTATGGAGG	CTGCCGGGGC AATAAGAACA GCTACCGCTC	300
O <b>RF</b>	N N F I	Y G G	C R G N K N S Y R S	100
R74593	TGAGGAGGCC	TGCATGCTCC	GCTGCTTCCG UCAGCAGGAG AATCCTCCCC	350
ORF	E E A		C F R Q Q E N P P I	117
R74593 ORF	TGCCCCTTGG P L G	CTCAAAGGTG S K V	GTGGTTCTGG CCGGGGCTGT TTCGTGATGG	133
R74593	TGTTGATCCT	TTTCCTGGGG	AGENTECATG GTETTACTGA TTCCGGGTGC	450
ORF	C * S F	S W G	A S M V L L I P G G	150
R74593	CAAGGAGGAA	CCAGGAGCGT	GCCCTGCGGA NCGTCTGGAG CTTCGGAGAT	r 500
ORF	K E E	P G A C		• 167
	GACAAGGGNT Q G			510 169

R74593 - Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)
ORF - EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

R35464	GGCCGGGTCGT	TICTCGCCTG	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC 50
N39798			TGGGANTC	GCTGCTCCTC	TCTGGGGTCC 28
H94519	GCNGCG-CGT	THNTCGCHT-	GCTGGGA-TC	GCTGCACCTC	TOTGGGGTCG 47
R74593 corr.					
Consensus	GGCCGGGTCGT	TICICGCCTC	GCTGGGA-TC	GCTGCTCCTC	TCTGGGGTCC 30
Translation	A G S F		L G S	LLL	s g v -3
. ranslation	x G 3 :	<b>2</b> 6 7			•
225464	***********	ACCGAGAACG	CACCATCCAC	GACTTOTGCC	TGGTGTCGAA 100
R35464	1GGCCGGCCG	ACCCACAACC	CAGCATCCAC	GACTTCTGCC	TGGTGTCGAA 77
N39798	TGG-CGGCCG	, ACCUAGAAC	CAGCATCCAC	CACTTCTCCC	TGGTGTCGAA 96
H94519	NGG-CGGCCC	ACCGAGAACC	CAGCATCCAC	CAC.ICIGCO	1001010010
R74593 corr.			- 010010000	CACTECTOCC	TGGTGTCGAA 99
Consensus			CAGCATCCAC	GACTICIOCC	Y S K 15
Translation	LAAS	REB	Z I H	D E C T	1 1 2 13
					0101100001 150
R35464	GGTGGTGGG	AGATTCCGG	G CCTCCATGCC	TAGGTGGTGG	TACAATGTCA 150
N39798	GGTGGTGGG	AGATGCCGG	G CCTCCATGCC	TAGGTGGTGG	TACAATGTCA 127
H94519	GGTGGTGGG	AGATGCCGG	G CCTCCATGCC	TAGGTGGTGG	TACAATGTCA 146
R74593 corr.					
Consensus	GGTGGTGGG	AGATECCEG	G CCTCCATGCC	TAGGTGGTGG	TACAATGTCA 149
Translation	2 Y Y	RCR	A S M E	BHH	<u> </u>
			_		
R35464	CTCACCGAT	CTGCCAGCT	G TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC 200
	CTCACCCAT	CTGCCAGCT	G TTTGTGTATG	GGGGCTGTGA	CGGAAACAGC 177
N39798	CIGACGGAIG	CIGCCAGCI	G TITGTGTATG	CCCCTCTC	CGGAAACAGC 196
H94519					GC 2
R74593 corr.			G TTTGTGTATG	CCCCCTCTCI	• • •
Consensus	CTGACGGAT				G N S 48
Translation	D G S	COL	EXXG		<b>2 2</b>
					•
R35464	AATAATTAC	C TGACCAAGG	A GGAGTGCCTC	AAGAAATGT	CCACTGTCAC 250
R35464 N39798	AATAATTAC	C TGACCAAGG	A GGAGTGCCTC	: AAGAAATGT(	CCACTGTCAC 22/
	AATAATTAC	C TGACCAAGG C TGACCAAGG	IA GGAGTGCCTC IA GGAGTGCCTC	: AAGAAATGT( : AAGAAATGT(	G CCACTGTCAC 227
N39798	AATAATTAC AATAATTAC AATAATTAC	C TGACCAAGG C TGACCAAGG C TGACCAAGG	ia ggagtgcctc ia ggagtgcctc ia ggagtgcctc	: Aagaaatgt( : Aagaaatgt( : Aagaaatgt(	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52
N39798 H94519 R74593 corr.	AATAATTAC AATAATTAC AATAATTAC	C TGACCAAGG C TGACCAAGG C TGACCAAGG	ia ggagtgcctc ia ggagtgcctc ia ggagtgcctc	: Aagaaatgt( : Aagaaatgt( : Aagaaatgt(	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249
N39798 H94519 R74593 corr. Consensus	AATAATTAC AATAATTAC AATAATTAC AATAATTAC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG	iA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC	: AAGAAATGT( : AAGAAATGT( : AAGAAATGT( : AAGAAATGT(	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52
N39798 H94519 R74593 corr.	AATAATTAC AATAATTAC AATAATTAC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG	iA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC	AAGAAATGT AAGAAATGT AAGAAATGT AAGAAATGT	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65
N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I	ia ggagtgeete ia ggagtgeete ia ggagtgeete ia ggagtgeete e e c l	AAGAAATGTO AAGAAATGTO AAGAAATGTO AAGAAATGTO K K C	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65
N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IC E E C L IC TGGCCACCAC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO K K C	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGAG	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IC TGGCCACCAC IC TGGCCACCAC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO K K C CAGGANATGC CAGGANATGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGAG C ACGGGTGAG	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IC TGGCCACCAC IC TGGCCACCACCACCCC IC TGGCCACCACCCACCCCCCCCCCCCACCACCCACCCACCC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO K K C C ANGGNATGC CAGGNATGC CAGGNATGC CAGGNATGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGAG C ACGGGTGAG C ACGGGTGAG C ACGGGTGAG	A GGAGTGCCTC A GGCCACCAC A GGCCACCAC A GGCCACCAC A GGCCACCAC A GGCCACCAC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO K K C  CAGGANATGC CAGGANATGC CAGGANATGC CAGGANATGC CAGGANATGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 102
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG	A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC E E C L C TGGCCACCAC C TGGCCACCAC C TGGCCACCACCACCCC C TGGCCACCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 102 CA GCGGATTCCT 102 CA GCGGATTCCT 299
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG	A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC E E C L C TGGCCACCAC C TGGCCACCAC C TGGCCACCACCACCCC C TGGCCACCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 102
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG	A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A TGGCCACCAC C TGGCCACCAC	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC CAGGANTGC ANGANTGC CAGGANTGC CAGGANTGC ANGANTGC ANGANTGC ANGANTGC	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A GCGGATTCCT 102 CA GCGGATTCCT 299 A D S 3 32
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGA	A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A GGAGTGCCTC A TGGCCACCAC C TGGCCACGAT	ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGCO CAGGANTGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 353
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGA	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IC TGGCCACCAC IC A GGCAGGAT IC A AGGCAGGAT IC A AGGCAGGAT	AGANATGTO AGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGCO AA	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 CA GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 5 32 CC ACTTCAGCGA 353 CC ACTTCAGCGA 352
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGA	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA TGGCCACCAC IA TGGCCACCAC IA TGGCCACCAC IA T S IA AGGCAGGAT	AGANATGTO AGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGTO AAGANATGCO AA	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 CA GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 351 CC ACTTCAGCGA 352 CC ACTTCAGCGA 345
N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC CTGTCCCAA CTGTCCCAA CTGTCCCAA	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I C ACGGGTGAG C ACGGGTGA	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA TGGCCACCAC IA TGGCCACCAC IA TGGCCACCAC IA T S IA AGGCAGGAT IA	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A D S 3 32 CC ACTTCAGCGA 353 CC ACTTCAGCGA 353 CC ACTTCAGCGA 345
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC E N A CTGTCCCAA CTGTCCCAA CTGTCCCAA	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I  C ACGGGTGAG C ACGGGTG	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA TGGCCACCAC IA TGGCCACCAC IA TGGCCACCAC IA T S IA AGGCAGGAT IA	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A D S 3 32 CC ACTTCAGCGA 351 CC ACTTCAGCGA 326 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 346
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Consensus	AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAG	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K !  C ACGGGTGAG C ACGGGTG	IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA GGAGTGCCTC IA TGGCCACCAC IA TGGCCACCAC IA TGGCCACCAC IA T S IA AGGCAGGAT IA	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 CA GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 351 CC ACTTCAGCGA 352 CC ACTTCAGCGA 345
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAGAATGC AG	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG L T K I  C ACGGGTGAG C ACGGGTG	A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  C TGGCCACCAC  C TGGCCACGAT  C A GGCAGGAT  GA AGGCAGGAT  C D	AGANATGTO AGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO ANGANATGTO CAGGANTGC CA	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 353 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 346 CC ACTCCAGCGA 348
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC E N A CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGG	A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  C TGGCCACCAC  C TGGCCACGAT  C A T S  C A A TAATTGC  AG AATAATTGC  AG AATAATTGC  A GGAAGTGCACGAT  C A A TAATTGC  A GAATAATTGC  A GAATAATTCC  A	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 5 32 CC ACTTCAGCGA 351 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 346 CC ACTCCAGCGA 348
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr Consensus Translation  R35464 R39798 R74593 corr Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC E N A CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU CTGTCCCAU	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGG	A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  A GGAGTGCCTC  C TGGCCACCAC  C TGGCCACGAT  C A T S  C A A TAATTGC  AG AATAATTGC  AG AATAATTGC  A GGAAGTGCACGAT  C A A TAATTGC  A GAATAATTGC  A GAATAATTCC  A	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 5 32 CC ACTTCAGCGA 351 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 346 CC ACTCCAGCGA 348
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC E N A CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA CTGTCCCAA	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGGGTGCCA C ACGGGTGAG C ACG	AGAGTAGATA  GAAGTAGCTC  GAAGTAGCTC  GAAGTAGCTC  GAAGTAGCTC  GAAGTAGCTC  GAAGTAGCACAC  GC TGGCCACCAC  GC TGGCCACCAC  GC TGGCCACCAC  GC TGGCCACCAC  GC TGGCCACCAC  GC TGGCCACCAC  GA AGGCAGGAT  GA AGGCAGGAT  GA AGGCAGGAT  GA AGGCAGGAT  GA AGGCAGGAT  GA AGGCAGGAT  AGGC	AGANATGTO AGANATGTO AGANATGTO AGANATGTO AGANATGTO AGANATGTO AGANATGTO AGANATGCO AGANAT	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A GCGGATTCCT 299 A D S 3 32 CC ACTCCAGCGA 351 CC ACTCCAGCGA 345 CC ACTCCAGCGA 346 CC ACTCCAGCGA 348
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R35464 N39798 H94519	AATAATTAC AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y  AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGGGTGCCA C ACGGTCCCA C ACGGTTCCCA C ACGGGTGAG C ACGG	IN GGAGTGCCTC IN GGAGTGCCTC IN GGAGTGCCTC IN GGAGTGCCTC IN GGAGTGCCTC IN TGGCCACCAC IN TGGCCACGAT IN TGGCCAGGAT IN TGGCAGGAT	CAGANATGTO CAGANATGTO CAGANATGTO CAGANATGTO CAGGANTGC CA	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 352 CC ACTTCAGCGA 352 CC ACTCCAGCGA 348 CC ACTCCAGCA 348 CC A
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTAC AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y  AGAGAATGC	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGGTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGTTCCCA C ACGGGTGAC C ACGGGTG	A AGCAGAT  A AGCAGGAT  A	CAGANATGTO CAGANATGTO CAGANATGTO CAGANATGTO CAGANATGTO CAGANATGCO CAGGANTGCO CAGGANTGCO CAGGANTGCO CAGGANTGCO CAGGANTGCO CAGGANTGCO CAGGANTGCO CACGANAC CT CT-GANGAC CT CT CT CT CT CT CT C	G CCACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 52 G CCACTGTCAC 52 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 A GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 352 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGA 348 H S S D 99 GN ATT 393 GC AGTCACTGGG 392 GC ATTCACTGGG 392 GC ATTCACTGGG 392 GC AGTCACTGGG 392
N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R74593 corr. Consensus Translation  R35464 N39798 H94519 R35464 N39798 H94519	AATAATTAC AATAATTAC AATAATTAC AATAATTAC AATAATTAC N N Y AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC AGAGAATGC E N A CTGTCCCAL	C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C TGACCAAGG C ACGGGTGAG C ACGG	A AGCAGAT  A AGCAGGAT  A	CAGAAATGTO CAGAAATGTO CAGAAATGTO CAGGAATGCO CAGGAATGCO CAGGAATGCO CAGGAATGCO CAGGAATGCO CAGGAATGCO CAGGAATGCO CACGGAATGCO CACGGAATGCO CACGGAATGCO CACCGAAGACO CACCGAAGACO CACCGACCAACCO CACCGCCAACCO CACCGCCAACCO CACCGCCAACCO CACCGCCCAACCO CACCGCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCAACCO CACCGCCCACCO CACCGCCACCO CACCGCCACCO CACCGCCCACCO CACCCCCCCCC CACCCCCCCCCC	G CACTGTCAC 227 G CCACTGTCAC 246 G CCACTGTCAC 249 A T V T 65 A GCGGATTCCT 300 A GCGGATTCCT 277 A GCGGATTCCT 296 CA GCGGATTCCT 296 CA GCGGATTCCT 299 A D S 3 32 CC ACTTCAGCGA 350 CC ACTTCAGCGA 345 CC ACTCCAGCGA 345 CC ACTCCAGCGGA 345 CC ACTCCAGCGGA 346 CC ACTCCACGGGA 346 CC ACTCCAGCGGA 346 CC ACTCCAGCGA 346 CC ACTCCAGCGA 346 CC ACTCCAGCGGA 346 CC ACTCCAGCGGA 346 CC ACTCCAGCGA 346 CC ACTCCAGCACA

R35464	
N397 <b>98</b>	COTTGO-GTG GAATCOTTTC CCACGCTGGN AATTTNGACG TTGAGAAGGA 421
H94519	CCT-GC-GTG -CATCCTT-C CCACGCTGGT ACTTT-GNCG 427
R74593 corr.	CCTTGCCGTG -CATCCTT-C CCACGCTGGT ACTTT-GACG TGGAGA-GGA 243
Consensus	COTTGCCUTG -CATCOTT-C CCACGCTGGT ACTTT-GACG TGGAGA-GGA 440
Translation	PCRASE PRWY F D V ER N 129
R35464	
N39798	AC 423
H94519	
R74593 corr.	ACTECTGEAA TAACTTEATE TATGGAGGET GEEGGGGGAA TAAGAACAGE 293
Consensus	ACTOCTGCAA TAACTTCATO TATGGAGGOT GOOGGGGCAA TAAGAACAGO 490
Translation	SCN NF: YGGC RGN KNS 145
R35464	
N39798	
H94519	
R74593 corr.	TACCGCTCTG AGGAGGCCTG CATGCTCCGC TGCTTCCGCC AGCAGGAGAA 343
Consensus	TACCGCTCTG AGGAGGCCTG CATGCTCCGC TGCTTCCGCC AGCAGGAGAA 540
Translation	YRSEEACMLRCFRQQEN 162
	•
R35464	********* ********* ********* *********
N39798	
H94519	
R74593 corr.	TOCTOCCOTG COCCTTGGCT CAAAGGTGGT GGTTCTGGCC GGGGCTGTTT 393
Consensus	TECTECCETG CECETTGGET CHANGGTGGT GGTTCTGGEC GGGGCTGTTT 590
Translation	PPLPLGS K V V V L A G A V S 179
R35464	
N39798	
H94519	
R74593 corr.	CGTGATGGTG TTGATCCTTT TCCTGGGGAG CNTCCATGGT CTTACTGATT 443
Consensus	CGTGATGGTG TTGATCCTTT TCCTGGGGAG CNTCCATGGT CTTACTGATT 640
Translation	* W C * S F S W G A S M V L L I 195
R35464	***************************************
N39798	
H94519	
R74593 corr.	CCGGGTGGCA AGGAGGAACC AGGAGCGTGC CCTGCGGANC GTCTGGAGCT 493
Consensus	CCGGGTGGCA AGGAGGAACC AGGAGCGTGC CCTGCGGANC GTCTGGAGCT 690
Translation	PGGKEEPGACPA*RLEUIII
R35464	•••••
N39798	•••••
H94519	
R74593 corr.	TCGGAGATGA CAAGGGNT
Consensus	TOGGAGATGA CAAGGGNT
	R R * Q G
KEY	
R35464 = Nucl	eic acid sequence of EST R35464 (SEQ ID NO.: 12)
N39798 - Nucl	eld acid sequence of EST N39798 (SEQ ID NO.: 17)
	eld acid sequence of EST H94519 (SEQ ID NO.: 16)
	- Correct d version of (SEQ ID NO.: 14) G at b.p. 114
	lucality and semisors for numer historia (SEC TO NO T)

Consensus = Nucelic acid sequence for numan bikunin (SEQ ID NO.: 3). Translation = Amino acid Translation of Consensus (SEQ ID NO.: 13).

The state of the s

Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin

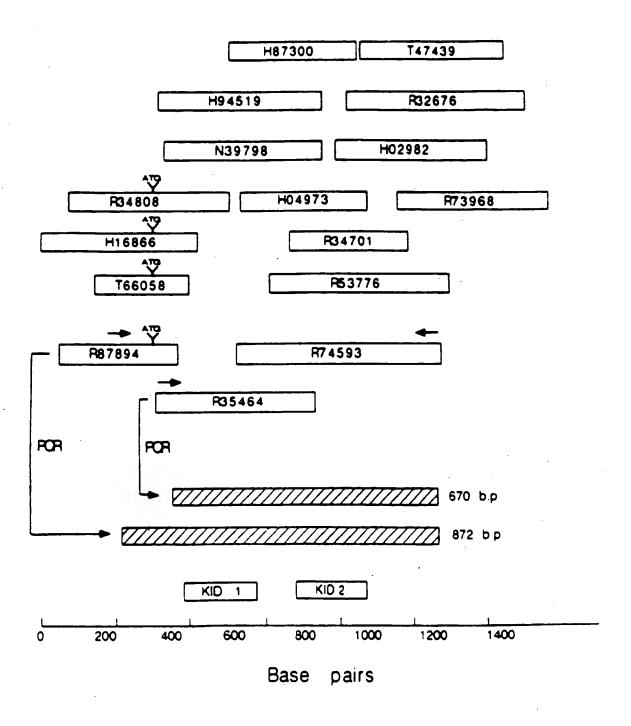
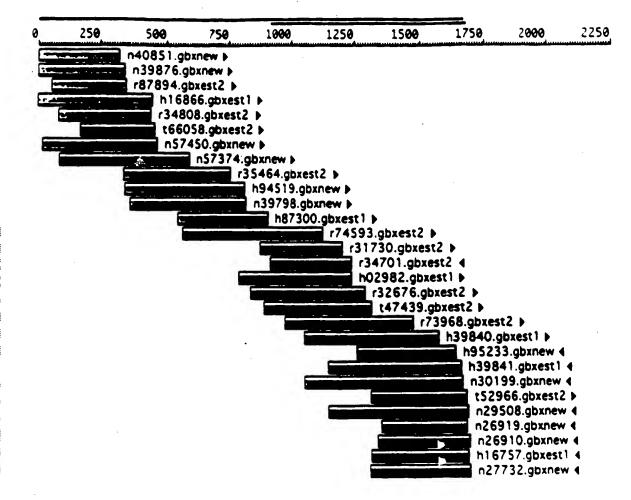


Figure 4B



### Figure 40

	1				50
Bikunin	scca	concesses	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N40851	GCGA	cetececes	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
<b>N39876</b>	GCSA	cereceses	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
R87894					
H16866	GGCGA	ככככככככ	TTGGGAGGTG	TAGCGCG.CT	CTGANCGGGN
R34838					
766058					
N57450			<b>:</b>	TAGCGCGGCT	CTGAACGCNA
N57374					
R35464					
H94519	• • • • • • • • • • • • • • • • • • • •				
N39798	• • • • • • • • • • • • • • • • • • • •				
H67300	• • • • • • • • • • • •				
R74593					
R31730					
R34701					
802982	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
R32676	• • • • • • • • • • • • • • • • • • • •				
747439	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • •		
R73968	• • • • • • • • • • • • • • • • • • • •				
HJ9840	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •		
95233	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • •		
E39841	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •	
N30:99	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
752966	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
N29508	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • •		
N26919	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
N26910	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •		
H:6757	• • • • • • • • • • • • • • • • • • • •				
427712					

	51	(002 0	,		100
Bikunin	- •	*********	CACCCCCCA	SSSCGCSAST	
N40851	NGAGNGGCCG				
N39876	SCA. GSGCCG			GGGCGCGAGT	
887894				SSSCCCSAST	
H: 6866				SGGCGCSAGT	
R34808	ANGGGCCG			GGSCN.GAGT	
	• • • • • • • • • • • • • • • • • • • •			<b></b>	GAGGAGEAGA
166058		• • • • • • • • • • • •	• • • • • • • • • • • •	• • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
NS7450		TTGAGTGTCG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
N57374	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •		AGA
R35464	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •			
H94519	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		
98 TECK	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
H87300	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
R74593					• • • • • • • • • • • • • • • • • • • •
R31730					
R34701					• • • • • • • • • •
HC2982					
R32676					
747439			· · · · · · · · · · · · · · · · · · ·		
273968					
H39840					
H95233					
H39841					
N30199					
752966					***********
N29508					
N26919	•				
N26910		• • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H16757				• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N27732			• • • • • • • •		• • • • • • • • • • •
		• • • • • • • • •			

Fi	gure	4C	(C	n't	)		
	:01						:50
BIKUNIN	CCCAGO	CATC	ccscc	CCGAS	AAGNC GGGC	GTCCCCACAC	
N40851						GTCCCCACAC	
N39876							TGAAGGTCCS
R87894						GTCCCCACAC	
H16866	CCCAGG	CATC	ccccc	CCGAG	AAGNC . GGGC	GTCCCCACAC	TGAAGGTCCC
R34808	CCCAGG	CATC	sesses	CCGAS	AAGNC, GGGC	STCCCCACAC	TGAAGGTCCC
166058							
N57450	CCCAGG	CATC	cccc	CCGAG	AAGNC . GGGC	GTCCCCACAC	TGAAGGTCCG
N57374	CCCAGG	CATC	ccccc	CCGAG	AAGNC . GGGC	GTCCCCACAC	TGAAGGTCCS
R35464							
H94519							
N39798	• • • • • •						
H87300		• • • •		• • • • •			
R74593		• • • •	• • • • •	• • • • •			
R31730							
R3470:		· ·	• • • • •				
HC2982							
232676	· • • • • • •		· · · · · ·				
747439	· · · · · · · ·		· · · · · ·				
R73968							
H39840							
H95233							
H39841	• • • • • • •						• • • • • • • • • • • • • • • • • • • •
N30199	• • • • • • •	• • •	· · · · ·	• • • •			
752966							
N2 9508	• • • • • • •	• • •	• • • • •	• • • •			
N26919	· · · · · · · ·			• • • •	• • • • • • • • • • •		
N2691C	• • • • • • •						
H:6757	• • • • • • •	• • • •	· · · · ·	• • • •	• • • • • • • • • •		

	ranse 4C	(Con't	)		
	151				200
Bikunir	GAAAGGCGAC	: TTCC56656C	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N40851	GAAAGGCGAC	: :::::::::::::::::::::::::::::::::::::			
N39876				GGCGGACCCT	
287894	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
H16866	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACG.T	CCCGGAGCN.
R34808	GAAAGGCGAC	TTCCGGGGGC		SGCGGACCCT	
166058					CCCGGAGCGT
N57450	GAAAGGCGAC	TTCCCGGGGGC	TTTGGCACCT	GGCGGACCCT	
N57374	- and accord	77006666		GGCGGACCCT	
R35464	•••••			•••••	
H94519					
N39798					
H87300					
R74593					
R31730	• • • • • • • • • • • • • • • • • • • •				
R34701	• • • • • • • • • • • • • • • • • • • •				
H02962					
R32676					
147439					
R73968					
H39840	• • • • • • • • • • • • • • • • • • • •				
H95233					
839841					
и30199					
752966	• • • • • • • • • • • • • • • • • • • •				
N29508					
N26919	• • • • • • • • • • • • • • • • • • • •				
N26910					
H16757					

	201	*			2 S C
Bikunin	CGSCACCISA	ACGCGAGGCG	CTCCATTGCG	CSTGCSTTTG	. AGGGGCTTC
N40851	COGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTNTG	. AGGGGCTTC
N39876	CGSCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	. AGGGGCTTC
R87894	COGCACCTGA	ACCCCAGGCG	CTCCATTGCS	CGTGCGTTTG	. AGGGGCTTC
H16866	.GGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CSTGCSTITG	. AGGGGCTTC
R34808	CCCCACCTGA	ACCCSAGGES	CTCCATTGCG	CGTGCSTNTG	GAGGGGCTTC
766058	CGGCACCTGA	ACCCGAGGE.	CTCCATTGCS	.GTGCGTGTG	MAGGCGCTTC
N57450	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	. AGGGGCTTC
N57374	CGGCACCTGA	ACGCGAGGC.	CTCCATTGC.	CGTGCGTTNG	. AGGGGCTTC
R35464					
H94519					
N39798					
H87300					
R74593					
R31730					
R34701			• • • • • • • • • • • • • • • • • • • •		
HC2382					
R32676					
747439					
373968					
H39840					
H95233					
H39841					
N3C199					
752966					
N29508					
N26919					
N26910					
H16757					
W27737					

•	•		•		
	251				300
grknuru	CCGCACCT G	ATCCCGAGAC	CCCAACGGCT	SGTGG CSTC	sc ts csts
N40851	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	accts.cass
N39876	CCGCACCT.G	ATCCCGAGAC	CCCAACGGCT	SGTGG.CSTC	50000.0000
P87994	CCSCACCT.G	ATCGCGAGAC	CCCAACGGCT	GCTNG.CGTC	GC.TM.CGCS
H16866	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTNG.CGTC	SC.TSSCGCS
234808	CCGCACCT.G	ATCCCGAGAC	CCCAACGGCT	GGTGGGCGTT	SC. TS
166058	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CSTC	GC. TG. CGCS
N57450	CCGCACCT.G	ATCSCGAGAC	CCCAACGGCT	SGTGG.CSTC	GCCTG.CGCG
N57374	CCGGAACTTG	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GC.TS.CGCS
R35464					
H94519					
N39798					
H87300					
A74593	• • • • • • • • • • • • • • • • • • • •				
R31730					
R34701	• • • • • • • • • • • • • • • • • • • •				
H05885	• • • • • • • • • • • • • • • • • • • •				
R32676					
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3968 רא		<b></b> .			
#39840	• • • • • • • • • • • • • • • • • • • •				
H95233					• • • • • • • • • • • • • • • • • • • •
H3984:					
N30199					
752966			· · · · · · · · · · · ·		
N29508					
N26919					
N26910					
H16757		· · · · · · · · · · · · · · · · · · ·			
N27732					

	301				350
Bikunin	to tossets	AGCT GGCCA	TGUCGCANT	cttsc ssec	T GAGGE GG
N40851	TC.TCGGCTG	AGET. SGNCA	TGTCG		
N39876	TC.TCGGCTG	AGCT.GGCCA	TGGCGCACT.	G.TGCGGNGC	T.GAGGE.S
R87894	TC.TCGGCTG	AGCTTGGCCA	TGGCGCANT.	GTTNC.SGGC	T. NAGGC . SG
H16866	TTCTCGGCTG	AGCT.GGCCA	TGGCGCANT.	GTTGC.GNGC	T.GAGGC.GS
R348C8	TETTEGGETG	AGCTGGGCCA	TGGCGCANTT	GTTGC.GGGC	T.GAGGC.GG
166058	TC.TCSSCTG	AGCT.GGCCA	TGGCGCANT.	GTTGC.GNGC	T.GAGGE.GG
N57450	TC.TCGGCTG	AGCT.GGCCA	TGGCGCANT.	GGTGC.GGGC	TTGAGGC.GG
N57374	TOOTOGGOTG	AGCT.GGCCA	TGGCGCANT.	GGTGCCGNGC	T.GAGGCCGG
R35464					650000
H94519					
N39798					
H87300					
R74593					
331730					
334701	• • • • • • • • • • • • • • • • • • • •				
402982					
832676		• • • • • • • • • • • • • • • • • • • •			
747439		• • • • • • • • • • • • • • • • • • • •			• • • • • • • • • •
R73968					• • • • • • • • •
H39840					
H95233	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •			
H39841	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	.:	• • • • • • • • • •	
N30199	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • •	• • • • • • • • • •
752966	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •			• • • • • • • • • •
N29508	• • • • • • • • • • • • • • • • • • • •		• • • • • • • •	• • • • • • • • •	• • • • • • • • • •
N26919	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
N26910	• • • • • • • • • •				
H16757	• • • • • • • • • • • • • • • • • • • •				
N27732					

	351				400
Bikunin	AC SG CS	TITCICS	cc tactass	A TOGET GE	: :::::::
R87894	ACG.				
H16866	ACCGNCGT	:::::::::::::::::::::::::::::::::::::::	cettectess	ATTOGOTTEC	TECETNEETS
234808	ACGCGGNCG.	.TTTTTTCSN	ccttcctccc	Attig.itg.	CONCICION
766058	CGGNCG.	TTTTCTCG.	CC.TGCTGGG	A.TCGCT.GC	T.CCTCTCT.
N57450	ANN.NGCCG.	זודכוכה.	cc.tectess	A.TOSCT.SC	t.cctctct.
N57374	AGGGCCGG		CCTTGCTGGS	A.TCGCT.GC	T.CCTCTCTG
R35464	GTCG.	<b>111</b> 0100 .	CCTGGCTGGG	A.TCGCT.GC	T.CCTCTCT.
H94519	.GCNGCGCG.	TTNNTCS.	CN. TGCTGGG	A.TCGCT.GC	A.CCTCTCT.
N39798			CTGGG	ANTCGCT.GC	t.cctctct.
H87300					
R74593					
R3:730					
R34701	• • • • • • • • • • • • • • • • • • • •				
H02982		· · · · · · · · · · · · · · ·			
932676	·····				
747439					
R73968					
H39840					
H95233					
839841					
N3C199					
752966					
N29508					
N26919	• • • • • • • • • • • • • • • • • • • •				
N26910					
H16757					
N27732					

. Fi	gure 4c	(Con't	)		
	401				450
Bikunin	GGGG TCCTG	G CSGCCGA	CCGA GAACG	CA GCA TCC	
H:6866	GGGGTTCCTS	GG . CSGCCSA	CCGA . GAACG	CA.GCA.TCC	AAGAATTTT
R34808	SGGGTTC . TG	GGGNGGCCGA	NCGA . SAACS	CAAGCA . TTC	ACGA
766058	6666.70075	S CSGCCSA	CEGA . SAACG	CA.GCA.TCC	ACGANTE CT
N57450	5566. 70073	G CGGCCGA	CCGA GAACG	CALGOA TOO	ACCACTT CT
N\$7374	- GGGG . TCCTG	G CSGCCGA	NCGAAGAANG	CA.GCAATCC	ANGAATTHCT
R35464	SGGG. TCCTG	G.CCGGCCGA	CCGA . GAACG	CA.GCA.TCC	ACGACTT CT
H94519	GGGG. TCGNG	GCGGCCGA	CCGA.GAACG	CA.GCA.TCC	ACGACTT CT
N39798	GGGG.TCCTG	G CGGCCGA	CCGA.GAACG	CA.GCA.TCC	ACGACTT CT
H87300	• • • • • • • • • • • • • • • • • • • •				
R74593	• • • • • • • • • • • • • • • • • • • •				
A3:730					
R34701	• • • • • • • • • • • • • • • • • • • •				
H05 885					
R32676					
747439					
R73968					
H3984C	• • • • • • • • • • • • • • • • • • • •				
H95233		• • • • • • • • • • • • • • • • • • • •			
H39841					
N30199	• • • • • • • • • • • • • • • • • • • •				
752966	•,•••••				
N29508	• • • • • • • • • • • • • • • • • • • •				
N26919	• • • • • • • • • • • • • • • • • • • •				
N26910	• • • • • • • • • • • • • • • • • • • •	· · · · · · · · · · · · ·	· · · · · · · · · · · · · · ·		
H16757	• • • • • • • • • • • • • • • • • • • •				
N27732					

	451				500
Bikanin	GCCTGGTGT	CSAAGST SS	TOGGCAGATO		CATGCCTA S
H16866	sec				
166058	TECTOSTOTT	CGAAGG			
N57450	GCCTGGTGT,	CGAAGST.SS	TOGGCAG		
857374	SCCTGGTSTT	CSAAAGTTSS	TOGGCANATT	ccscscctt	CATGNCTAAG
R35464	GCCTGGTGT.	CGAAGGT . SC			
h94519	GCCTGSTST.	CGAAGGT . SG			
H39798	GCCTGGTGT.	CGAAGGT.SG	TGGGCAGATG	cccc.cctc	CATGCCTA.G
H87300					
274593					
831730	• • • • • • • • • • • • • • • • • • • •				
R34701					
H02982	• • • • • • • • • • • • • • • • • • • •		,		
R32676	• • • • • • • • • • • • • • • • • • • •				
747439					· · · · · · · · · · · · · · · · · · ·
373968					
#3984C		• • • • • • • • • • • • • • • • • • • •			
H 62533	• • • • • • • • • • • • • • • • • • • •				
839841					
N30199	• • • • • • • • • • •				
752966	• • • • • • • • • • • • • • • • • • • •				
N29508	• • • • • • • • • • • • • • • • • • • •	· · · · · · · · · · · · · · ·			
N26919		• • • • • • • • • • •			
N2691C					
H16757					
N27732					

Fi	gure (	C	(Con't	)		÷
	501					55:
Bitunin	S TGGT C	ict /	ACANTGTEAC	TGACGGATCC	TOCCAGOTOT	TESTST ATS
N57374	GTTGGTTG	ict i	ANAATGTNAA	TTAANGATTO	TIGEMETET	TIGIGINATI
R35464	G.TGGT.G	ict /	ACANTGTCAC	TGACGGATCC	TGCCAGCTGT	TTSTGT.ATS
H94519	5.7557.0	ist /	ACANTGTOAC	TOACGGATCC	TGCTAGCTCT	TTSTST.ATS
N39798	G. TGST. G	ist /	CANTGTOAC	TGACGGATCC	TGCCAGCTGT	TIGTGT . ATG
H87300			· • • • • • • • • • • • • • • • • • • •			
R74593			. <b>. </b>	******		
R31730						
R347C:			<b></b>			
H02902						
R32676						• • • • • • • • • • • • • • • • • • • •
747439						
R73968						•••••
H3984C						• • • • • • • • • • • • • • • • • • • •
H95233						
239841						
N30199					• • • • • • • • • • • • • • • • • • • •	
752966					• • • • • • • • • • • • • • • • • • • •	
N29528					• • • • • • • • • • • • • • • • • • • •	
N26919					• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N2691C					• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H16757				• • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • •
N27732				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
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	551					
Bikunio	551 356657676	:a	CCCANACA	CC44-14-14		600
Bikunin NS7374	GGGGCTGTG				CCTGACCAAG	GA SGAGTGE
N57374	SSSSCTISTS SSSSCTNTS	TA A	ACGGAAANA	.CAATAATNA	CCTGACCAAG CCTGACCAAA	GA SGAGTGC GAAGNAAT
N57374 R35464	GGGGCTGTC GGGGCTNTT GGGGCTGTC	TA A Sa .	ACGGAAANA .CGGAAACA	.CAATAATHA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC
N57374 R35464 H94519	CGGGCTGTC CGGGCTSTC CGGGCTGTC	TA A SA . SA .	ACGGAAANA .CGGAAACA .CGGAAACA	.CAATAATNA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG CCTGACCAAG	GA GGAGTGE GAAGNAAT GA.GGAGTGE GA.GGAGTGE
N57374 R35464 H94519 N39798	GGGGCTGTG GGGGCTNTT GGGGCTGTG GGGGCTGTG	TA A SA . SA .	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA	.CAATAATHA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C	GGGGCTGTG GGGGCTGTG GGGGCTGTG GGGGCTGTG GATTGGGG	TA A SA . SA . SA . AC A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	.CAATAATHA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTNC
N57374 R35464 H94519 N39798 H8730C R74593	SGGGCTGTC GGGGCTGTC GGGGCTGTC GGGGCTGTC GATTCGGCA	TA A SA . SA . SA . AC A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA	CAATAATHA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTNC
N57374 R35464 H94519 N39798 H87300 R74593 R31730	GGGGCTGTG GGGGCTGTG GGGGCTGTG GGGGCTGTG GATTGGGG	TA A SA . SA . SA . AC A	ACGGAAANA .CGGAAACA .EGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTNC
N57374 R35464 H94519 N39798 H8730C R74593 R31730 R34701	GGGGCTGTC GGGGCTGTC GGGGCTGTC GATTCGGC	TA A  SA .  SA .  SA .  AC A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R31730 R34701 HC2982	GGGGCTGTC GGGGCTGTC GGGGCTGTC GATTCGGC	TA A SA . SA . SA . AC A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HG2982 R32676	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SATTCSGCA	TA A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	TA A	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HG2982 R32676 T47439 R73968	SGGGCTGTC GGGGCTGTC GGGGCTGTC GGGGCTGTC GATTCGGC/	TA A CA A CA A CA CA CA CA CA CA CA CA CA	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HG2982 R32676 T47439 R73968 E39840	GGGGCTGTC GGGGCTGTC GGGGCTGTC GATTCGGC	TA A	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 HC2982 R32676 T47439 R73968 H39841 H95233	GGGGCTGTC GGGGCTGTC GGGGCTGTC GGGGCTGTC	TA A SA	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA GGGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 E39840 H95233 E39841	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	FA A SA	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA .GGGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 E39840 H95233 E39841 N30199	SGGGCTGTC GGGGCTGTC GGGGCTGTC GGGGCTGTC	GA A A A A A A A A A A A A A A A A A A	ACGGAAACA .CGGAAACA .CGGAAACA .GGGAAACA .GGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HG2982 R32676 T47439 R73968 E39840 H95233 E39841 N30199 T52966	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	GRA A GRAND A	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA .GGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 HG2982 R32676 T47439 R73968 E39840 H95233 H39841 N3C199 T52966 N295G8	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	AC A	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 HC2982 R32676 T47439 R73968 H39841 H95233 H39841 N3C199 T52966 N295G8 N26919	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	TA A A A A A A A A A A A A A A A A A A	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA .GGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39841 H95233 H39841 N30199 T52966 N26919 N26910	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	TA A A GA	ACGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA .CGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 E39840 H95233 R39841 N30199 T52966 N29508 N26910 H16757	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	GA A GA	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA .GGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39841 H95233 H39841 N30199 T52966 N26919 N26910	SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC SGGGCTGTC	GA A GA	ACGGAAANA .CGGAAACA .CGGAAACA .CGGAAACA .GGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC

	601	- (C	а с	• •		
Bikunin		•				65C
R35464				CACAGAGAAT		
H94519	CTCAAGAAA				GCCACGGGTS	
N39798	CTCAAGAAA CTCAAGAAA				GCCACGGGTG	
H87300					GCCACGGGTG	
R74593	CTCAAGAAA				GCCACGGGTG	
R31730	CTCAAGAAA		ACTGI	CACAGAGAAT	GCCACGGGTS	ACCTGGCCAC
R34701	• • • • • • • • •		• • • • •	• • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
HC2982	• • • • • • • • •		• • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
R32676	• • • • • • • • •		• • • • •	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
T47439	• • • • • • • • • • • • • • • • • • • •		• • • • •	• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
R73968	• • • • • • • • • •		• • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H39840	• • • • • • • • • • • • • • • • • • • •		• • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H95233				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
H39841				• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
N3C199					• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
752966	• • • • • • • • • • • • • • • • • • • •				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N29508	• • • • • • • • • • • • • • • • • • • •					• • • • • • • • • • • • • • • • • • • •
N26919	• • • • • • • • • • • •					• • • • • • • • • • • • • • • • • • • •
N26910						• • • • • • • • • •
216757						• • • • • • • • • •
N27732						
	651					700
Bikunin		GCAGC	SGATT	Cetetatece	AAGTGCTCCC	700
Bikunin R35464	651 CAGCAGGAAT CAGCAGGAAT				AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG
-	CAGCAGGAAT	GCAGC	GGATT	cctctstccc	AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG
R35464	CAGCAGGAAT CAGCAGGAAT	GCAGC	GGATT GGATT	CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGC: GCAGC:	GGATT GGATT GGATT	cctctstccc	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGC	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCE GCAGCE GCAGCE	GGATT GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGC: GCAGC: GCAGC: GCAGC: GCAGC:	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31130	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCE GCAGCE GCAGCE GCAGCE	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGC	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGC	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R21730 R34701 H02982 R32676 T47439 R73968	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 E39841	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439 R73968 H39840 H35233	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 E39841	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 R94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439 R73968 H39840 H95233 R39841 N30199	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 A39841 N30199 T52966	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT GGATT GGATT GGATT GGATT GGATT GGATT GGATT GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439 R73968 H39840 H95233 R39841 N30199 T52966 N29508	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508 N26919	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI GCAGCI	GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31130 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508 N26919 N26910	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCI GCAGCI GCAGCI	GGATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG

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	ATTCT. SAA		G CGATATSTT.	CAACTATG	AAGAATACTS
H8730C R74593	ATTET GAA	G ACCACTCCA	G CGATATGTT.	CAACTATG	AAGAATACTG
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R35464	CACCGCCAA GCACCGNCAA	CGNATT		,	800 DADDD TTDD
R35464 H94519	CACCGCCAA GCACCGHCAA GCACCGCCAA	CGNATT.CAC	TGGGCCTG	C.GTG.CAT.	800 DADDD TTDD
R35464 H94519 N39798	CACCGCCAA GCACCGCCAA GCACCGCCAA	CGCATT.CAC CGCAGT.CAC	TGGGCCTG	C.GTG.CAT.	800 CCTT CCCAC CCTT.CCCAC
R35464 H94519	CACCGCCAA GCACCGCCAA GCACCGCCAA .CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC	TGGGCCTG TGGGGCCTTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873CO R74593	CACCGCCAA GCACCGCCAA GCACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC	TGGGCCTG TGGGGCCTTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	800 CCTT CCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 R31730	CACCGCCAA GCACCGCCAA GCACCGCCAA .CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC	TGGGCCTG TGGGGCCTTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 R31730 R347C1	CACCGCCAA GCACCGCCAA GCACCGCCAA .CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC	TGGGCCTG TGGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 a74593 a31730 R347C1 H02982	CACCGCCAA GCACCGCCAA GCACCGCCAA .CACCGCCAA	CGNATT CAC CGCAGT.CAC CGCAGTNCAC CGCAGTNCAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 A31730 R347C1 H02982 R32676	CACCGCCAA GCACCGHCAA GCACCGCCAA .CACCGCCAA .CACCGCCAA .CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 R74593 R31730 R347C1 H02982 R32676 T47439	CACCGCCAA GCACCGHCAA GCACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 a74593 R31730 R347C1 H02982 R32676 T47439 R73968	CACCGCCAA GCACCGHCAA GCACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CAC CGCAGT.CAC CGCAGTNCAC CGCAGTNCAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTT.CCCAC CCTTT.CCCAC
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R35464 H94519 N39798 H873C0 A74593 A31730 R347C1 H02982 R32676 T47439 R73968 H39840 495233	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 R74593 R31730 R347C1 H02982 R32676 T47439 R73968 H39840 H95233 H39841	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CAC CGCAGT.CAC CGCAGTNCAC CGCAGTNCAC	TSGGCCTG TSGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 a74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 495233 H39841 N30199	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN	800 CCTT CCCAC CCTTTCCCAC CCTTTCCCAC CCTTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 A31730 R347C1 H02982 R32676 T47439 R73968 H39840 495233 H39841 N3C199 T52966	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCC.TTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN	800 CCTT CCCAC CCTTTCCCAC CCTTTCCCAC CCTTT. CCCAC
R35464 H94519 N39798 H87300 A74593 A31730 R34701 H02982 R32676 T47439 R73968 H39840 495233 H39841 N30199 T52966 N29508	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TSGGCCTG TSGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTTTCCCAC CCTTTCCCAC CCTTT. CCCAC
R35464 H94519 N39798 H87300 A74593 A31730 R34701 H02982 R32676 T47439 R73968 H39840 495233 H39841 N30199 T52966 N29508 N26919	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	800 CCTT CCCAC CCTTTCCCAC CCTTTCCCAC CCTTT. CCCAC
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R35464 H94519 N39798 H87300 A74593 A31730 R34701 H02982 R32676 T47439 R73968 H39840 495233 H39841 N30199 T52966 S29508 N26919 S26910 R16757	CACCGCCAA GCACCGCCAA CACCGCCAA CACCGCCAA CACCGCCAA	CGNATT CGCATT.CAC CGCAGT.CAC CGCAGTNCAC CGCAGT.CAC	TGGGCCTG TGGGCCTTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN CCGTG.CAT.	860 CCTT CCCAC CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC

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H94519	GCTGGTACT				
N 39798	GETGGNAAT	T INGACGTTGA	GAAGGAAC		
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	GGAGGCT GC			TACCGCTC T	GAGGAGGCCT
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Bikunin H87300	GGAGGET GE GGAGGETTGE	CCCCCCAAT CCCCCCAATN	AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTCTT TACCGCTC.T	GAGGAGGCCT TAGGAGGCCT GAGGAGGCCT
Bikunin H87300 R74593	GGAGGET GE GGAGGETTGE GGAGGET.GE	CGGGGCAAT CGGGGCAATN CGGGGCAAT.	AAGAACAGNT AAGAACAG.C	TACCGCTC T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730	GGAGGET GE GGAGGETTGE GGAGGET.GE	CGGGGCAAT CGGGGCAATN CGGGGCAAT	AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T	GAGGAGGCCT TAGGAGGCCT GAGGAGGCCT
Bikunin H87300 R74593 R31730 R34701	GGAGGET GE GGAGGETTGE GGAGGET.GE	CGGGGCAAT CGGGGCAATN CGGGGCAAT	AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGACGEET
Bikunin H87300 R74593 R31730 R34701 HC2982	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGSGGCAAT CGGGGCAATN CGGGGCAAT.	AAGAACAGNT AAGAACAG.C G.C AAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGACGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAATN CGGGGCAAT.  CGGGGCAAT.	AAGAACAGNT AAGAACAG.C G.C AAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAATN CGGGGCAAT.  CGGGGCAAT.	AAGAACAGNT AAGAACAG.C G.C AAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAATN CGGGGCAAT.  CGGGGCAAT.	AAGAACAGNT AAGAACAG.C G.C AAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGSGGCAAT CSGGGCAAT CGGGGCAAT 	AAGAACAG.CG.CAAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGSGGCAAT CSGGGCAAT CGGGGCAAT 	AAGAACAG.CG.CAAGAACA.NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG.CG.CG.CAAGAACA.NC.AAGAACA.C.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG.CG.CAAGAACA.NC AAGAACA.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGACGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG.CG.CAAGAACA.NC AAGAACA.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 R39840 H95233 H39841 N30199 T52966 N29508 N26919 N26910	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGSGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG.CG.CAAGAACA.NC AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
Bikunin H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 R39840 H95233 H39841 N30199 T52966 N29508	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGSGGCAAT CSGGGCAAT. CGGGGCAAT.	AAGAACAG.CG.CAAGAACAG.C AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET

1,7	gure 40	(Con't	.)		
	90:		•		950
Bikunin	SCA TGCT		sc		CA GCAGGA
H87300	.GCA.T				
R74593	.GCA .TGCT	כ כפכדפהדדכם	sc		. CA . GCAGGA
R31730	. SCA . TGCT		GC		
.R34701			<b>G</b> C		. CAAGCAGGA
HO2982	. GCG . TGCT			CTCTTCCAGG	CCA.GCAGGA
R32676	GCA TGCT	: :::::::::::::::::::::::::::::::::::::	cc		.CA.GCAGGA
T47439	TGCAGTGCT	CGCTGCTTCC	GC		.CA.GCAGGA
R73968					· · · · · · · · · · · · · · · · · · ·
HJ9840	••••••				
H95233	• • • • • • • • • • •				
H39841	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •		
N30199	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
752966	••••••				
929508	• • • • • • • • • • • • • • • • • • • •				
N26919	• • • • • • • • • • • • • • • • • • • •				
N26910			• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
H16757	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		
N27732	••••••	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •		
31 8 0 0 1 0	951	<i></i>			:000
31KUN1N R74593	GAA TOCTOO	ccisccccii	GGCTCAAAGG	TGGTGGTTC	TGG CGGGGC
R74593	GAA TCCTCC	CCTGCCCCTT	GGCTCAAAGS	TEGTEGTTC.	TGG CGGGGC TGGGCGGGC
R74593 R31730	GAA TCCTCC GAA.TCCTCC GAA.TCCTCC	CCTGCCCCTT	GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC
R74593 R31730 R34701	GAA TOCTOO GAA.TOCTOO GAA.TOCTOO AAANTOCTOO	CCTGCCCCTT CCTCCCCCTT	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTCC	TGG CGGGGC TGG_CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982	GAA TCCTCC GAA.TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC	CCTGCCCCTT CCTCCCCCTT CCTCCCCCTT	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTCC TGGTGGTTCC TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676	GAA TCCTCC GAA.TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC	cctocccctt cctocccctt cctocccctt cctocccctt	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982	GAA TOCTOC GAA.TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CSGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439	GAA TOCTOC GAA.TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968	GAA TOCTOC GAA.TOCTOC GAA.TOCTOC AAANTOCTOC GAA.TOCTOC GAA.TOCTOC GAA.TOCTOC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 R339840	GAA TOCTOC GAA.TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 R39840 H95233	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CSGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841 N30139	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 R339840 H95233 H39841 N30199 T52966	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 R339840 H95233 H39841 N30199 T52966 N29508	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	CCTGCCCCTT CCTGCCCCTT CCTGCCCCTT CCTGCCCCTT	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC
R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841 N30139 T52966 N29508 N26919	GAA TCCTCC GAA.TCCTCC AAANTCCTCC GAA.TCCTCC GAA.TCCTCC GAA.TCCTCC	ccreccerr ccreccerr ccreccerr ccreccerr ccreccerr	GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG GGCTCAAAGG	TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC. TGGTGGTTC.	TGG CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC TGG.CGGGGC

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#### (Con't) :00: 1252 TOTT COTGA TOGTCTTCAT CC T CTTCC TOGG AGCCT CC ATGGTC BIERUTU R74593 IGITECGIGA IGGIGITGAT CCTT...TCC IGGGGAGCNT CC.ATCGICT R31730 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGGGAGCCT CC.ATGGTC. R34701 TGTT.CGTGA TGGTGTTGAT CCCTCCTTCC CGGG.AGCCT CCCATGGTCC H02982 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATCGTN. R32676 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. T47439 IGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. R73968 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. H39840 H95233 ......... H39841 ...... N30199 .... T52966 ..... N29508 N26919 ..... N26910 ..... H16757 ....... N27732 .... 1051 1100 Sikunin TACC TGAT | CCGGGTGGCA CGGAGG AAC C AGG AGCG TGCCCTGCGC R74593 TAC..TGATT CCGGGTGGCA AGGAGG.AAC C.AGG.AGCG TGCCCTGCGG R31730 TACC.TGAT. CCGGGTGGCA CGGAGGGAAC-C.AGGGAGCG TGCCCTGCGC R34701 TACCCTGAT: CCGGGTGGCA CGGAGG.AAC CCAGG.ANCG TGCCCTGCGC HO2982 TACC. TGAT. CCGGGTNGCA CGGAGG. AAC C. AGGGAGCG TGCCCTGCGN R32676 TACC.TGAT. CCGGGTGGCA CGGAGG.AAC C.AGGGAGCG TGCCCTGCGC T47439 TACC.TGAT. CCGGGTNGCA CGGAGG.AAC C.AGG.AGCG TGCCCTGCGC R73968 TACC.TGAT. CCGGGTGGCA CGGAGG.AAC C.AGG.AGCG TGCCCTGCGC H39840 H95233 **339841** N3C:99 752966 ...... N29508 N26919 N26910 ...... H16757 צריקא .....

Figure

<b>3</b> 13	igure	4C	(Con't	:)		
	1101		-	•		
Bikunı	n ACCG :	:: c	GAGCTCCGGA	GATGATAAGO	AGCAGCTGG	1150
R7459	ANCS.T	CT.C	GAGCTTCSGA	GATGACAAGO	CHT	TGAAGAAC
R3173	ACCS.:	ctes (	GAGCTCCGGA	GATGACAASS	GAGCAGCTGG	CTCAACAAC
R3470;	ACCG.T	ct.c d	SAGCTCCGGA	GATGACAAGG	. AGCAGCTGG	
H02982	ACCS.T	CTNG (	AGCTCCGGA	GATGACAAGG	. AGCAGCTGG	.TGAAGAAC.
R32676	ACCG T	CT66 (	AGCTCCGGA	GATGACAAGG	GAGCAGCTGG	TGAAGAAC.
747439	ACCG.T	ct.c c	AGCTCCGGA	GATGACAAGG	AGCAGCTGG	.TGAAGAAC.
R73968				GATGACAAGG		.TGAAGAAC.
H39840	ACCGGT	T.G C	AGCTCCGGA	GATGACAAGG	AGCAGCTGG	.TGAAGAAC.
H95233						.TGAAGAAC.
H39841					• • • • • • • • • • • • • • • • • • • •	•••••••
NJ0199	ACCG.TO	T.G G	AGCTCCGGA	GATNACAANG	. AGCAGCIGN	*********
752966			• • • • • • • • • •			. TGAAGAACC
N29508	• • • • • • • •		• • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •
N26919	· · · · ·				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •
N26910					• • • • • • • • • • • • • • • • • • • •	
H16757					••••••	
N27732						
					• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
	1151					
BIRGUIN	ACATATO	: : ::	ST GACCS	SSCIET FEE	C AAGAGG A	1200
R31730	ACATATG:	ite et	GTTGACCS	NCCTSTTCSC	C. AAGAGG. A	CT GSSGAA
RJ4701	ACATATG	וכ כז	GT.GACCS	CCCTGT . CGC	C. AAGAGG. A	TIGGGGGAA.
H02982	ACATATST	.c c <b>:</b>	GT.GACCS	NCCIGITEGN	C. AAGAGG. A	CT.GGGGAA.
R32676	ACATATGT	יום כד	GTTGACCG	CCCTGTTCGC	C. AAGAGGGA	LINGGGGAAA
T47439	ACATATGT	.c ct	GT.GACCG	202 707 202	C. AAGAGG. A	NIGGGGGAA.
R73968	JOHINIO!	.c cr	GT.GACCG (	CCCTGT.cac	C AACACC A	
H39840	ACATATST	.0 07:	GT.GACCG	ממי למלכני	C. AAGAGG. A	C:.GGGGAA.
н95233						
H3984:					CCAAAAGG.A	
N30199	ACATATST	.c c10	ST. GACCS	COINT COC	C. AÁGAGG.A	T. SGSGAA.
752966			• • • • • • • •			
N29508					C.AAGAGG.A	• • • • • • • • • • •
N26919		· ·			C.AAGAGG,A	TT.SSG.AA.
N26910	· · · · · ·				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •
H16757	• • • • • • • • •			* * * * * * * * * *	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •
W27777						

Fi	igure 40	(Con't	.)		
	1201				125:
Bikunir	GGGAGGGG	AGACTAT G	TOT GA GCT	TITITE AA	A TAGA GG
R31730	.GGGAGGGG	; A			
R34701	. GGGAGGGS.	AGACTAT.G.	TGT.GA.GCT	TITITIAA	A TA
HC2982	GCGGAGGG.	AGATTAT .G.	TGTTSA.GTT		
R32676	GGGGAGGGG	AGANTATTGT			
747439	.GGGAGGG.	AGACTAT.G.		TTTTTT AA	
R73968	.GGGAGGG.	AGACTAT.G.	TGT.GA.GCT		
H39840	GGGAGGG.	AGACTAT.C.	TST.SA.GCT		
H95233					
H39841	. GGGAGGGGA	AMACHAT.G.	TOT GAACCT		
N30199	. GGGAGGNG.	AGACTAT.G.	TGT . AA . GCT	TTTTTTAA	A. TAGAGG
752966	• • • • • • • • • • • • • • • • • • • •				
N2 9508	. GGGAGGGG.	AGACTAG.	TGT . GA . GCT	TTTTTT AA	A.TAGAGG
NS 6919		• • • • • • • • • • • • • • • • • • • •			
N26910		:			
H16757		••••••			
N27732	• • • • • • • • • • • • • • • • • • • •	••••••	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
0	1251				1,300
Bikunin R32676	SATTGACTC	SCATTIC A		TTAGGG CT	GAGGTCTSTT
747439	GNTTGANTTC		GTTGATCCAT	TTAGGGGGNT	GAG
R73968	GATTGACTC.		GT.GATC.A.	TTAGGGCT	
H39840		.GGATTTG.A		TTAGGGCT	GAGGTCTGT?
H95233	GATTGACTO.		GT.GATC.A.	TTAGGGCT	
H39041	GATTGACTC.	CC12222	<b>. .</b> .	TTAGGGCT	
N30199	GATTGACTC.	.GGATTTG . A		TTAGGGCT	
752966		.GGATTTGGA		TTAGGGCT	GAGGTCTGTT
N29508	GATTGACTC.	.GGATTTG.A			• • • • • • • • • • • • • • • • • • • •
N26919				TTAGGGCT	SAGGTCTSTT
N26910			• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H16757				• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N27732				• • • • • • • • • • • • • • • • • • • •	*.* * * * * * *
			* * * * * * * * * *	• • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
	1301				
Bikunin	TETETEGGAS	GTAGGACGGC	-:	S TO TOSCA	: 35:
747439	TETETNEGAG	STAGSACGA		J .C .CCCA	SSGATSSS
R73968				SCICITOCA	*****
H3984C	TETETEGGAG	GTAGGACGGC	1501700 00	S. TC. TOSCA	. 305A (6666
H95233	NCTCTGGGAG	NTAGGACGGC	Tacattagen	G. TO. TOGGA	. 3344 . 333 .
H39841	TONOTOGGAS	STAGGACGGC	TGCTCCTCTC	S. TC. TSSCA	COCATOC
N30199	TOTOTOGGAG	STAGGACGGC	7507700.70	G. TC. TSSCA	CCCATCCC
752966				- TO TOOCA	COLLEGE.
N2 9508	TETETSSGAS	STASSACSGE	TOUTTEAL TO	G. TC. TGGCA	
N26919					. 3007 . 300
N26910			• • • • • • • • • • • • • • • • • • • •		*********
H16757			<u>.</u>	S.TC.TSSCA	
827732				SETECTIONCA	ACCUATOCO.

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figure 4C (C n't)
          :351
 Bikunin TTTG CTTTG G AAATCCTC T AGGAGGCT CCTCCT CGC ATGG CC TG
  R73968 TITG.CTTTG GGAAATCCTC TINGGAGGCT CCTCCTTCGC ATGGGCCTTG
  H39840 TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG
  H95233 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  H39841 TITG.CITTG G.AAANCCNC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  M30199 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTTCGC ATGG.CC.TG
  152966 TITG.CTTTG G.AMATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  N29508 TITG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  N26919
         ......GAGGCT CCTCCT.CGC ATGG.CC.TG
  N26910 .....CTTTT GNAAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 H16757 ITTGCCTTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N27732 TTTG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG
         1401
Bikunin CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTC
 R73968 CAGT.CINGS CAGCANCCCC CGAGTTTTTT TCCTTCGCTG ATCCGATTTC
 H39840 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H95233 CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H39841 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC
 N30199 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 T52966 CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N29508 CAGI.CI..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
N26919 CAGT.CTTGG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC
N26910 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTC
H16757 CAGINETICS CAGCAGACCE CGAGITGITT .CC.TCGCTG ATC.GATITC
N27732 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC
        1451
Bikunin TTT CCTCCA GGTAG AGT TTTC TTTG CTTATGTTGA ATTCCATTGC
R73968 ITTTCCTCCA GGTAAGAATT TTTCTTTT
H39840 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
H95233 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
H39841 TTT.CCCCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ANTCCATTGC
N30199 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
T52966 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
N29508 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
N26919 TIT.CONCCA GGTAG..AGT TITC.TITG. CITATGTTGA ATTCCATTGC
N26910 TTT.CCTCCA GGTAG..ACT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
H16757 ITTACCCCCA GGTAG. AGT ITTCCTTTCN CTTATGTTGA ATTCCATTCC
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N27732 ITT.CCTCCA GGTAG..AGT ITTC.TTTG. CITATGTTGA ATTCCATTGC

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:50:
                                                         1550
 BIRUNIN CICITITE CT CATCACAGAA GEGATGETEG AATCGETTEE TETGETE ST
  H95233 CTCTTTI.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTI.GT
  H39841 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  NJ0199 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  T52966 CICITIT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  N29508 CTCTTTLCT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTL.GT
  N26919 CTCTTTT.CH CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  N26910 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  H16757 CICITITACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  N27732 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
         1551
                                                       1600
 Bikunin CIGATTIATG G TITTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
  H39840 CTGATTTATG GGTTTTTTT AAGTAT
 H95233 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 H39841 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 NJ0199 CTGATTTATG G..TTTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 T52966 CIGATITATE G... TITTITT AAGTATAAAC AAAAGTTITI TATTAGCATT
 N29508 CIGATITATE G. . TITTITT AAGTATAAAC AAAAGTITTI TATTAGCATT
 N26919 CIGATITATO G...TITITI AAGTHTAAAC AAAAGTITIT TATTAGCATT
 N26910 CTGATTTATG G..ITTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 H16757 CTGATTTATG G..TTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
 N27732 CTGATTTATG G..TTTTTTT AAGTATAAAC AAAAGTTTTT TATTAGCATT
         1601
Bikunin CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 H95233 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAA
 H39841 CTGAAAGAAG GAAAGTAAAN TGTACAAGTT TAATAAAAAG GGGCCTTCCC
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 T52966 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N29508 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
 N26919 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N26910 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
H16757 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
N27732 CTGAAAGAAG GAAAGTAAAA TGTACAAGTT TAATAAAAAG GGGCCTTCCC
        1651
BURUNIN CTITAG ART AAAAAAAAAA AAAAAAAAA AAAAAAAAA
H39841 CTTTAA.
N30199 CTTTAG.AAT AAA
T52966 CTTTAGGAAT NAAAANAAAA AAGGGTG
N29508 CTTTAG. AAT AAATTTCAGC ATGTGCTTTC AA
S26919 CTTTAG.AAT AAAAAAAAA AAAAAAAAA A
N26910 CTTTAG. AAT AAATTTCAGC ATGTGCTTTC AAAAAA
H16757 CTTTAG.AAT AAAAAAAAA AAAAAAAA AAAAAA
N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAA AAAAAAAAA
```

EST	consens	HLRAEADGVS	RLLGSLLLSG	VLAADRERSI	HDFCLVSKVV	GRCRASMPRW	50
EST	consens	WYNVTDGSCQ	LEVYGGCDGN	SMNYLTKEEC	LKKCATVTEN	ATGDLATSRN	100
EST	consens	AADSSVPSAP	RRQDSEDHSS	DMFNYEEYCT	ANAVTGPCRA	SFPRWYFOVE	150
EST	consens	RNSCNNFIYG	GCRGNKNSYR	SEEACHLRCF	ROQENPPLPL	GSK <u>YVVLAGL</u>	200
EST	consens	EVMVLILELG	ASMVYLIRVA	RRNOERALRT	VWSSGDDKEO	LVKNTYVL	248

cDNA translation																	c -	
cDNA translation	TGA1	CGC	GAG D	ACC(	NS:	G G	CIG W	GTC W	IGCG R	T (	GCC L	TGC R	GCG V	TCT <sup>o</sup> S	CGG( A	CTG. E	A -	\$ 3 30
cDNA translation	GCT:	SGC(	atg H	GCG A	CAG(	etgt L	GCC	G G	etga L	G R	GCG(	SAGC S	CGG R	GCC A	F F	CIC	G A-	103 ·13
cDNA - translation	CCC1	GCT L	eccc c	ATC(	SCT(	ECTC L	CTC	TC1 S	G G	G 1	CCT L	GGC A	JGC A	CGA	CCG R	AGA E	A :	.53
cDNA translation	CGC/ R	\GCJ	TCC H	ACG	ACT1 F	CTG	CCI	GG1 V	rgtc S	G	aagg K V	TGG V	TGG G	GCA R	GAT	GCC F	:G 2	203
cDNA translation	GGC	S	atg M	CCT	AGG1 R	TGGT W	GG1	raci	NTG V	T	CAC1 T	GAC D	GGA G	TCC S	TGC	CAC Q	E I	253 38
cDNA translation	TGT1	TG1 V	GTA Y	TGG G	GGG(	CTGT C	GAC D	G G	N N	S	GCN N	UT/ N	Y Y	CC1	GAC T	CA K	\G	303 54
cDNA translation	GAGG	GAG1 E (	GCC L	TCA K	AGA. K	MTG C	TG(	CA T	CTG1 V	C	ACA(	EAG!	n a	cci	NCG(	GGT( G	GA D	353 71
cDNA translation	CCT	SGC(	T T	AGC S	AGG R	aatg n a	CA	GCG A	GAT1 D	rc s	CTC' S	rgt( V	P P	AG' S	A TGC	TCC P	CA R	403 88
cDNA translation	GAA(	SGC.I	NGGA D	TTC S	TGA E	AGAC D	CA(	CTC S	CAG( S	CG D	ATA M	TGT F	TCAA N	CT.	ATG E	AAG E	**	453 104
cDNA translation	Y	TGC:	ACCG T A	CCA	ACG I A	CAGT	CA T	CTG	GGC(	CT	TGC C	CGT R	GCA1	cc	TTC F	P	CG R	503
cDNA translation	CTG W	GTA Y	CTTT F	GAC D	GTG V	GAGA E P	. GG	N N	TCC S	TG C	CAA N	TAA N	CTT(	I	CTA Y	TGC G	AG G	553 138
cDNA translation	GCT C	GCC R	0000 0	CAJ N	K K	.GAAC N	S AG	CT) Y	ACCG R	CT S	CTC	AGC	eagg E a	C C1	GCJ :	NTG(	etc L	603 154
cDNA translation	CGC R	<b>16</b> C C	TTCC F f	GC(	CAGO	AGG/ E	KD /	UNTO	CTC P P	; ; ; ;	CTC L	SCC(	CTT L	G G(	S	XXX X	GGT Y	653
cDNA translation	GGT 	GGT V	TCT	G GC	666( 6	; ;	T T	GT 7	GAT(	GT Y	GT'	TGA	TCCT	C T	TCC L	TGG G	GA C	; 703 198
cDNA translation	CC1	CCA	TGG'	r ct	VCC.	TGAT	C C:	SSG V	TGG(	CAC F	GG.	AGG R	AACC N (	ea g	GAG E	CGT R	GC:	753 204
cDNA	CTC	ccc	ACC	G TC	TGG.	AGCT	T C	GGA	GAT	GA								732 21

CDNA	GCACGAGTTG	GGAGGTGTAG	CGCGGCTCTG	AACGCGCTGA	GGGCCGTTGA 50
CDNA	GTGTCGCAGG	CGGCGAGGGC	GCGAGTGAGG	AGCAGACCCA	GGCATCGCGC 100
CDNA	GCCGAGAAGG	CCGGGCGTCC	CCACACTGAA	GGTCCGGAAA	GGCGACTTCC 150
SONA	CCCCCTTTC	GCACCTGGCG	GACCCTCCCG	GAGCGTCGGC	ACCTGAACGC 200
CONA	CACCCCCTCC	ATTCCCCCTC	CCCCTTGAGG	GCCTTCCCGC	ACCTGATCGC 250
	Characterist	ATTOCOCOTO	cocorrance	CCCTCTCCCC	TGAGCTGGCC 300
CDNA					
CDNA					TOGCCCTGCT 350
translation	HAQL	CGL	RRS	RAFL	A L L -11
CONA	GGGATCGCTG	CTCCTCTCTG	GGGTCCTGGC	GGCCGACCGA	GAACGCAGCA 400
					ERS:
	• • •				
40NA	*******		TOCALCOTOS	TOCCCACATO	CCGGGCCTCC 450
cranatacion	H D F.	C L V	2 K A A	GRC	R A S 23
					AGCTGTTTGT 500
translation	M P R W	WYN	VID	G S C Q	L F V 40
CONA	GTATGGGGGC	TOTGACGGAA	ACAGCAATAA	TTACCTGACC	AAGGAGGAGT :::
Tona landa	GINIGOGGC	. Olancoom	C N N	v i t	K E E C 57
crausistion	1 4	CDGN	3 11 11	1 5 1	K E E C 3.
					TGACCTGGCC 600
translation	LKK	CAT	V T E N	A T G	D L A 73
CDNA	ACCAGCAGGA	ATGCAGCGGA	TTCCTCTGTC	CCAAGTGCTC	CCAGAAGGCA 650
translation	TSRN	A A D	s s v	PSAP	R R Q 9,0
					•
-044		C1.CC1.CBCC1		CARCTATORA	GAATACTGCA 700
CDNA	GGATTCTGAA	GACCACICCA	CONTRIGIT	CANCINION.	GARIACIGCA 100
translation	D S E	D H S S	DHE	NYE	E Y C T 107
CDNA	CCGCCAACGC	AGTCACTGGG	CCTTGCCGTG	CATCCTTCCC	ACGCTGGTAC 750
translation	ANA	v : 3	PCRA	SFP	R W Y 123
~0W	*****	ACACCAACTC	CTCCAATAAC	********	GAGGCTGCCG 800
CDNA	i.:GACGIGG	NONCONNEC	C.3CM1MC		C C P 140
translation	FDVE	R N S	Сии	F 1 1 0	G C R 140
			•		
					CTCCGCTGCT 850
translation	G N K	N S Y R	3 2 2	A C M	L R C F 157
					•
CDNA	TOCGOORGE	GGAGAATOOT	CCCCTGCCC	TTGGCTCAN	GGTGGTGGTT 900
					<u>v v v</u> :73
crensiation	K Q Q	E 10 P			
	•				
CDNA	CTGGCGGGGG	: TGTTCGTGAT	GGTGTTGAT	CTCTTCCTG	GAGCCTCCAT 950
translation	LAGI	F V M	7 : :		3 A S M 190
					· · · · · · · · · · · · · · · · · · ·
			- caloscatoca	CCACGAGGG	+ CC^CTCCCC
-0111	*****			I CCAGGAGG	i occerococy
CDNA	GGTCTACCTC	ATCCGGGTGG			
cDNA translation	GGTCTACCTC	ATCCGGGTGC	N S S N	Q E R	A L R T 207
cDNA translation	GGTCTACCTC	ATCCGGGTGC	N	Q E R	A L R T 207
translation	<u> </u>	R V /		Q E R	A L R T 207
translation cDNA	CCGTCTGGAC	R V / G CTCCGGAGA1	A R R N GACAAGGAG	Q E R AGCTGGTGA	A L R T 207 A GAACACATAT 1050
translation cDNA	CCGTCTGGAC	R V / G CTCCGGAGA1	A R R N GACAAGGAG	Q E R AGCTGGTGA	A L R T 207
cona cona translation	CCGTCTGGAC	T R V A	A R R N GACAAGGAGG D K E (	Q E R C AGCTGGTGA Q L V K	A L R T 207 A GAACACATAT 1050 N T Y 203
translation  cDNA  translation  cDNA	CCGTCTGGAC V W S GTCCTGTGAC	T R V A	A R R N GACAAGGAGG D K E (	Q E R C AGCTGGTGA Q L V K	A L R T 207  A GAACACATAT 1050  N T Y 223
cona cona translation	CCGTCTGGAC V W S GTCCTGTGAC	T R V A	A R R N GACAAGGAGG D K E (	Q E R C AGCTGGTGA Q L V K	A L R T 207 A GAACACATAT 1050 N T Y 203

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CDNA	ATGTGTGAGC	TTTTTTTAAA	TAGAGGGATT	GACTCGGATT	TGAGTGATCA	1150
CDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
CDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
CDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
CDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
CDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCTGA	1400
CDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
CDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
CDNA	AATAAATTTC	CAGCATGTTG	CTTTCAAAAA		AAAA	
1550						

FC9						
EST consens			MLR	AEADGVSRLL	GSLLLSGVLA	-:
PCR clone			MAQLCGL	RRSRAFLALL	GSLLLSGVLA	-1
ACDNA clon			MAQLCGL	RRSRAFLALL	GSLLLSGVLA GSLLLSGVLA GSLLLSGVLA	-1
FCT conservation	******					
EST consens	ADRERSINDE	CLVSKVVGRC	RASMPRWWYN	VIDGSCQLFV	YGGCDGNSNN	50
PCR clone	ADRERSINDE	CLVSKVVGRC	RASMPRWWYN	VIDGSCQLEV	YGGCDGNSNN	50
ACDNA clone	ADRERSINDE	CLVSKVVGRC	RASMPRWWYN	VTDGSCQLFV	YGGCDGNSNN	50
EST consens	YI TEERCI KY	CATHENATO	D7.1.#CDV3.10	ccimentiane		
PCP close	VIGERECTER	CHIVIERAIG	DEATSKNAAD	22AL2VE KKŐ	DZEDHZZDWE	100
PCR clone	ILIKEECLKK	CATVIENATG	DLATSRNAAD	SSVPSAPRRQ	DSEDHSSDMF	100
AcDNA clone	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAPRRQ	DSEDHSSDMF	100
EST consens	NYEEYCTANA	VTGPCRASEP	RWYFDVERNS	CHNETYGGCR	CHENCYPORT	150
PCR clone	NYEEYCTANA	VTGPCRASER	SMALDALONG	CANETYCCCE	CHANCABEE	150
ACDNA clone	NYTEYCTANA	UTCDCDA CED	UMIT DA FULL	CHAPTIOGCK	CHANGER	.30
	MISSICIAMA	VIGPCRASEP	KMISDAFIN2	CNNFIIGGCR	GNENSTRSEE	150
EST consens	ACHLRCFRQQ	ENPPLPLGSK	VVVLAGLEVM	VLILFLGASH	YYLIRVARRN	200
PCR clone	ACMLRCFROO	ENPPLPLGSK	VVVLAGLEVM	"T.T.ET.GASM	WYT TRULBRA	200
CDNA clone	ACMI BCEROO	PURRICEK	IRRII I CI CI CI N	111 11 51 51 61	- TABLE NO MARKET	200
	vermuce voo	ENPPLPLOSK	YYYLAGLEYA	VILLERIGASH	VYLIKVARRN	200
ST consens	QERALRTVWS	SGDDKEQLVK	NTYVL			225
CR clone	OERALRTVWS	EGD	<del>-</del>			213
CDNA clone			NEVUI			
	Aniannut 1 m2	2000VEG FAK	MITAR			225

## Purification of Placental Bikunin using Superdex 75 Gel-Filtration

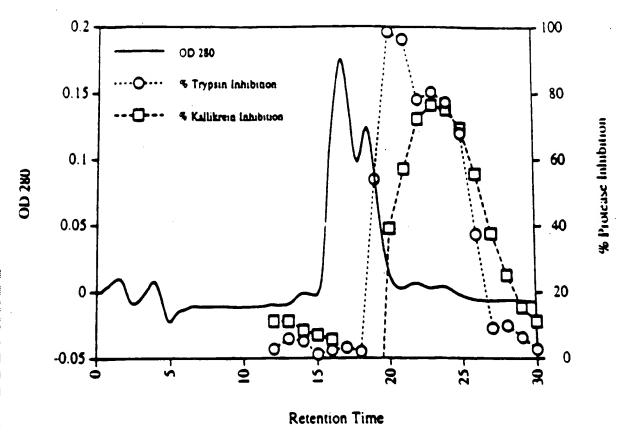


FIGURE 5



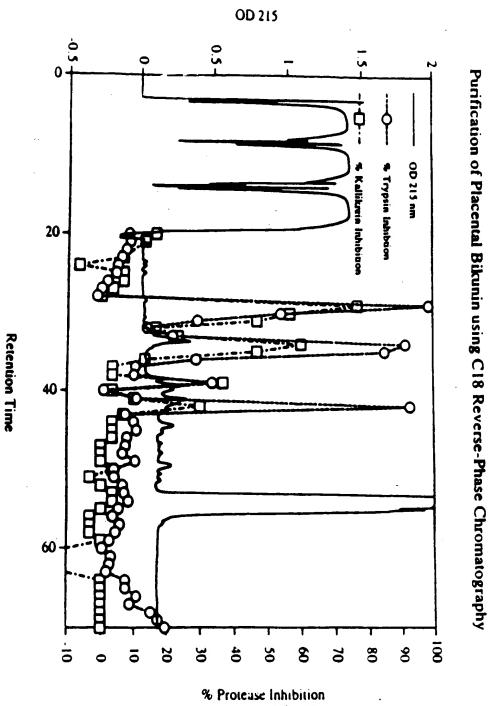


Figure 7

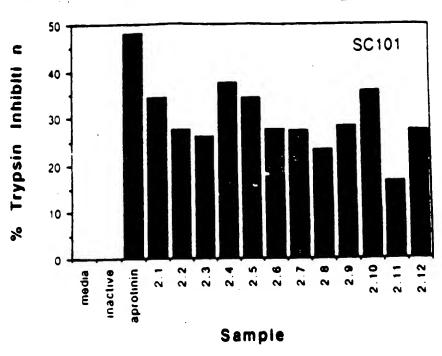
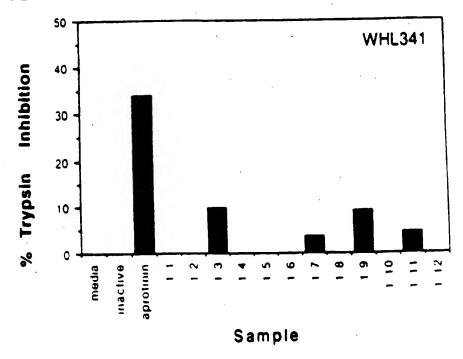
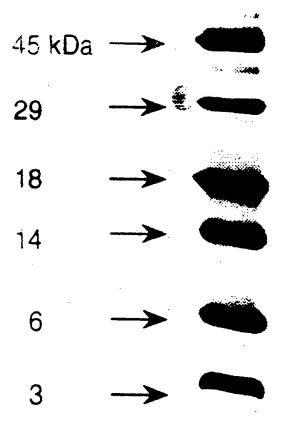
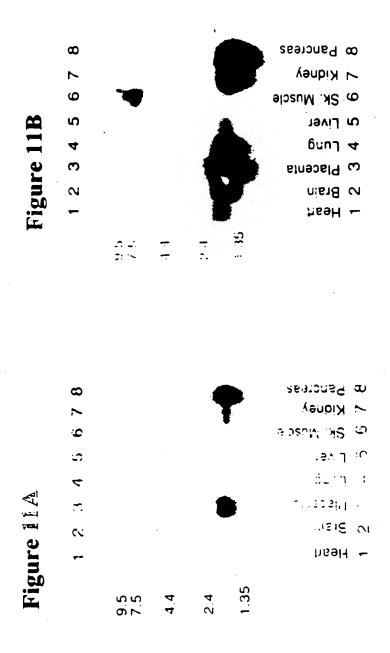


Figure 8B



### Figure 10





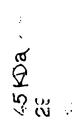


### 2 3 4

## Figure 12B

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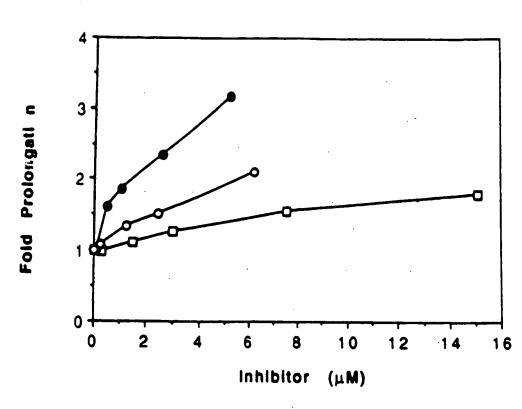


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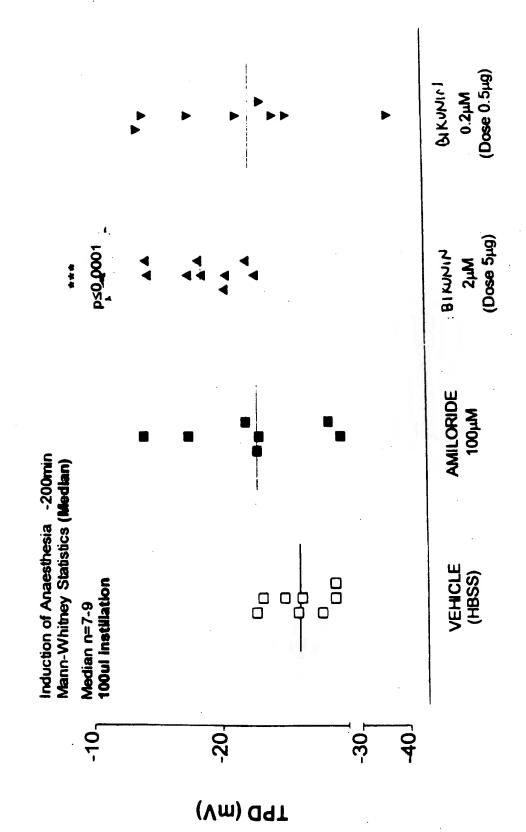
(:)

45 kDa 29 18 14 6

Figure 14

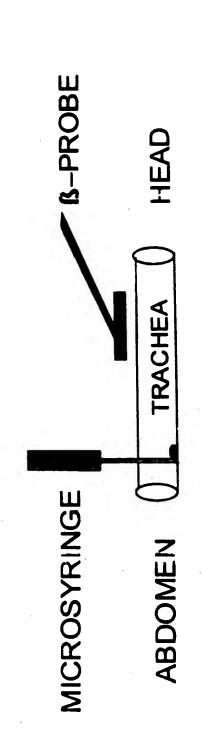


(0.2-2uM) and amiloride (100uM) on tracheal potential difference (TPD) 3 hours post treatment Figure 15: The effect of BIKUNIN



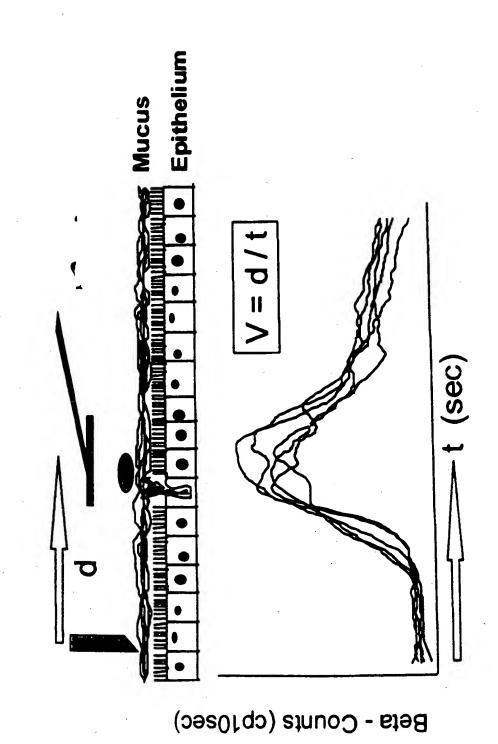
TREATMENT

Figure 16 (a): Diagram to show the arrangement of needle and Beta probe.

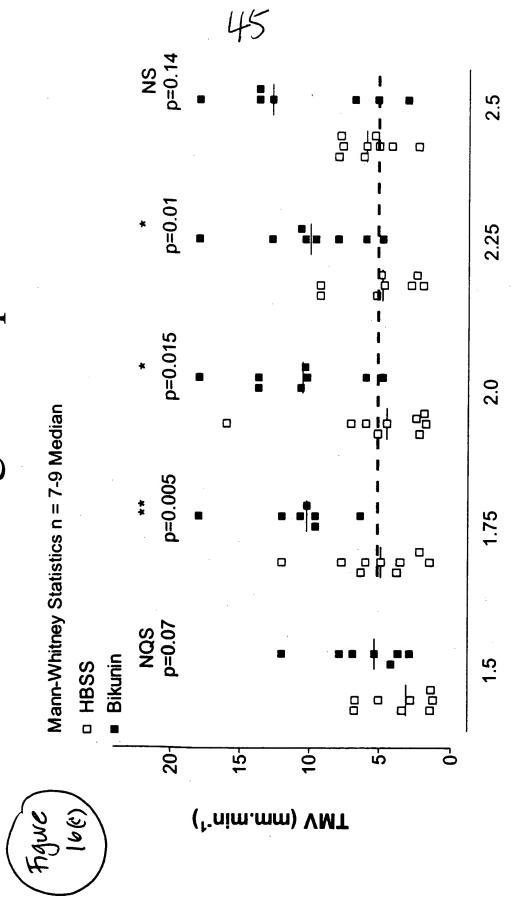


# Longitudinal view

Figure 16 (b): Counts detected by the probe as the <sup>32</sup>P-labeled Saccharomyces cerevisiae are transported along the tracheal mucociliary layer.



# Sustained Increase in Tracheal Mucus Velocity In Vivo in Guinea Pig in Response to Bikunin



TIME (HOURS) FROM TOPICAL TREATMENT

(70nM) on sodium dependent current in cultured normal Figure 17: Short circuit current (Isc) trace to show the action of human bronchial epithelial cells in vitro BIKUNIN

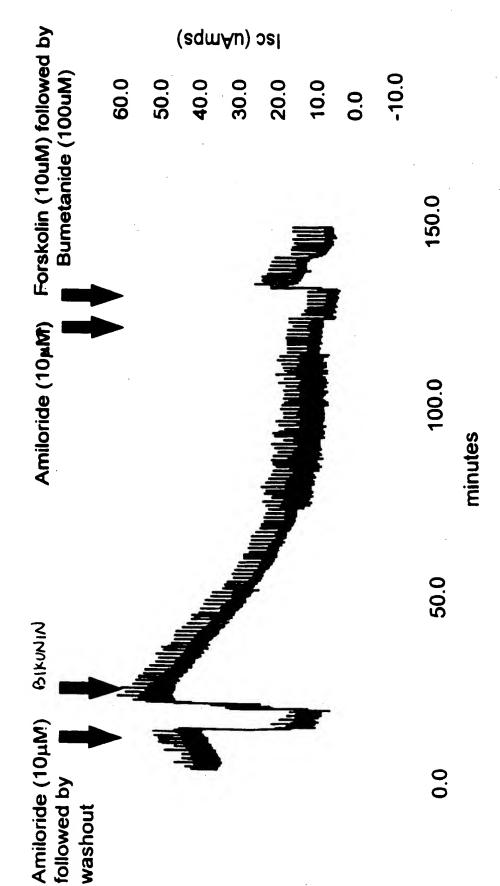
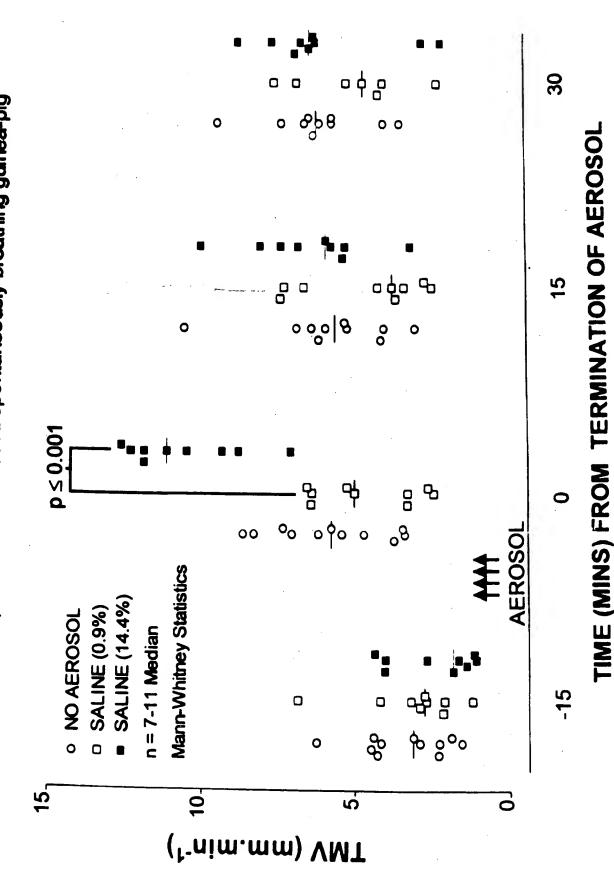
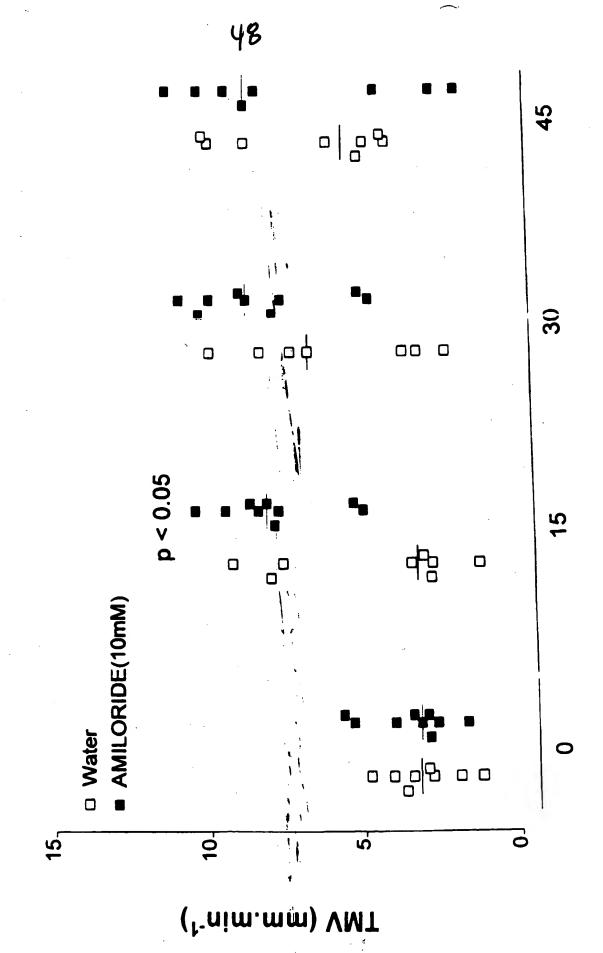
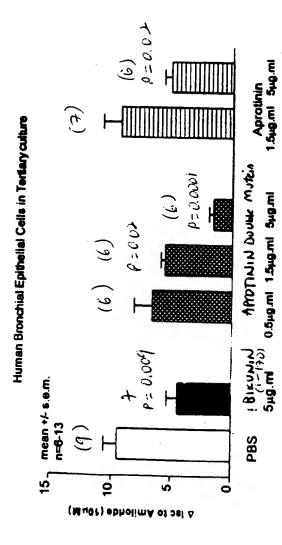


Figure 18 : The effect of a 5 min aerosol of hypertonic saline (14.4%) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig Figure 19 : The effect of a 20 min aerosol of amiloride (10mM) on tracheal





(5ug/mL) and Aprotinin (5 ug/mL) inhibit sodium dependent short circu current (Isc) in normal human bronchial epithelial cells in vitro at 90 Figure 20: Aprotinin double mutein (0.5 - 5 ug/mL), Bikurin (1-170) minutes following treatment.

(1 mg/mL) on sodium dependent current in cultured cystic fibrosis human Figure 21 Short circuit current (Isc) trace to show the action of aprotinin bronchial epithelial cells in vitro

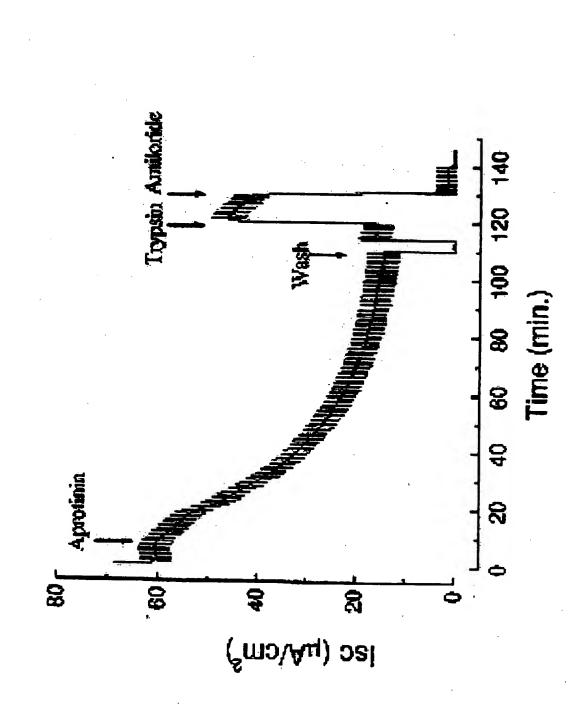


Figure 22: 9mg CHO mBikunin (1-170) aerosol (3 ml. of 3 mg/ml.) increased tracheal mucus velocity in sheep (n=6) at 0, 0.5, 3, compared to animals (n=6) receiving PBS vehicle

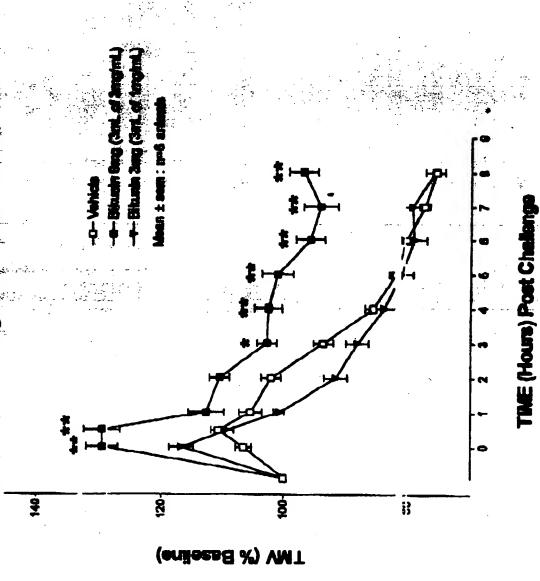


Figure 23: The effect of a 30 minute pre-treatment of Bikunin (50 amiloride (30uM) in cultured guinea-pig tracheal epithelial cells and 10 ug/mL) on the short circuit current ( $\Delta$  Isc) response to

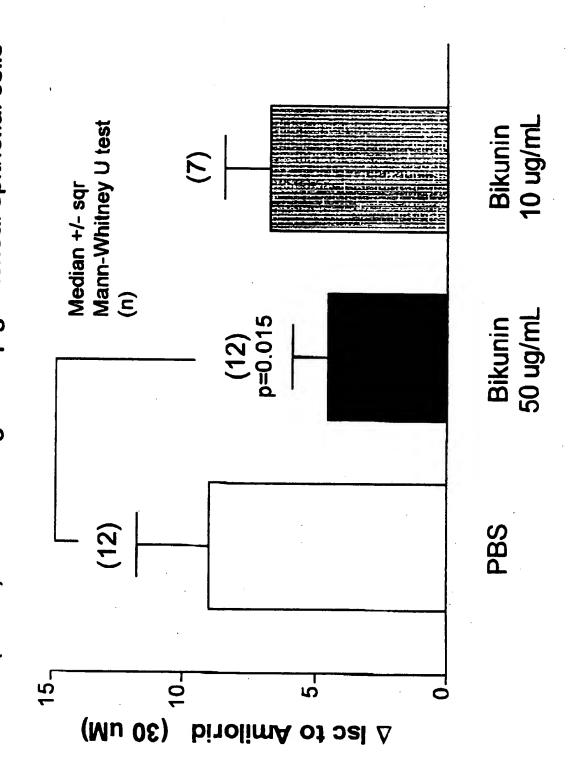


Figure 34: The effect of a 90 minute pre-treatment of Bikunin (100 and 50 ug/mL) on the short circuit current (A Isc) response to amiloride (10 uM) in cultured Ovine tracheal epithelial cells

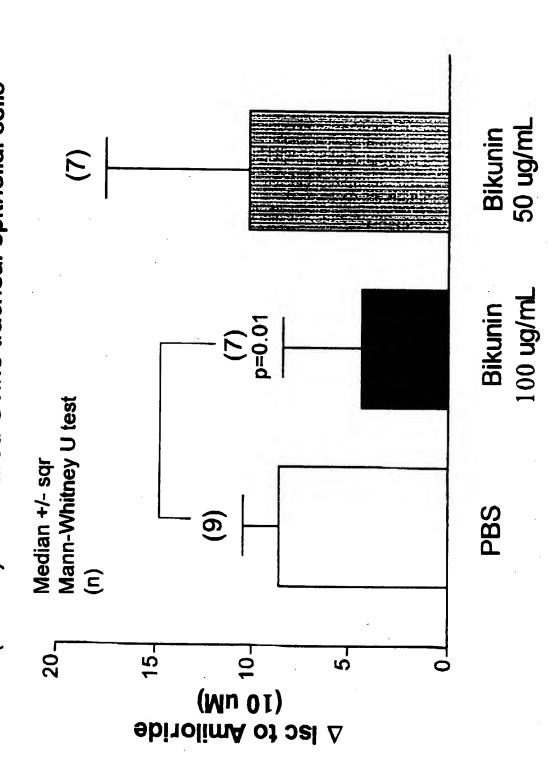


Figure 354): The Effect of LPS (0.03 mg/mL x 10 min) on neutrophil numbers in bronchoalveolar lavage fluid (BALF) of the guinea-pig 24 hours post challenge

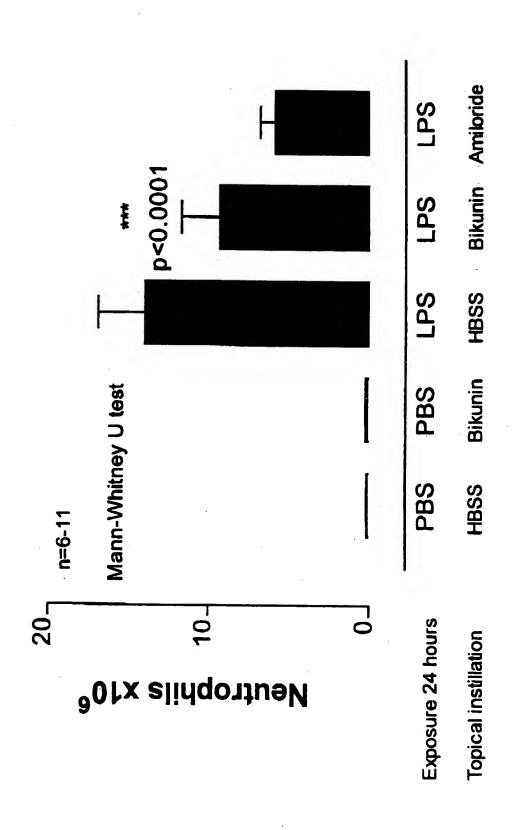
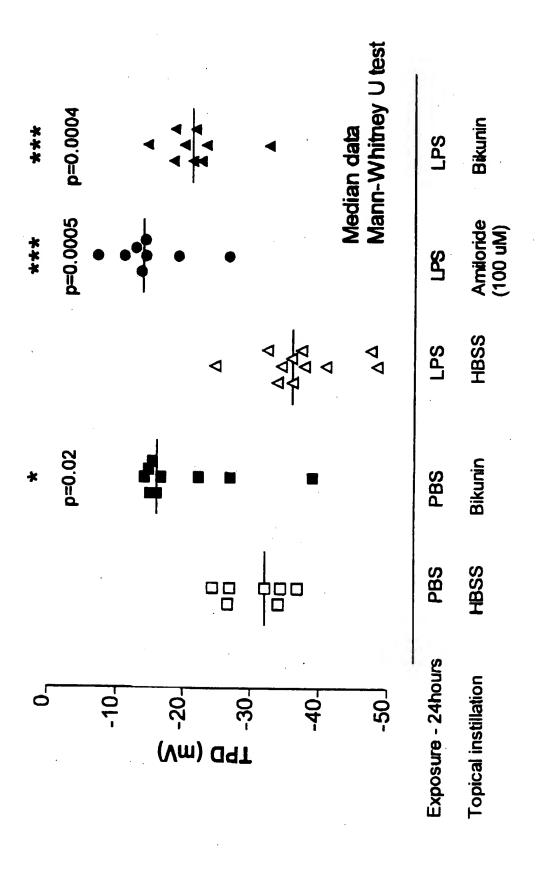
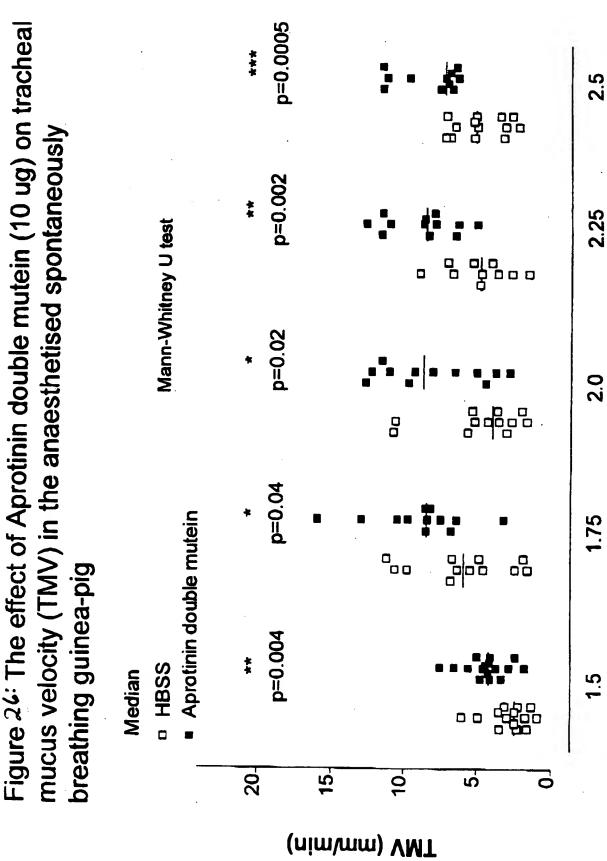


Figure 25(4): The Effect of Bikunin (50 ug/mL) on Tracheal Potential Difference (TPD) in Guinea-Pigs pre-exposed to LPS (0.03 mg/mL x 10 min)





TIME (HOURS) FROM TOPICAL TREATMENT

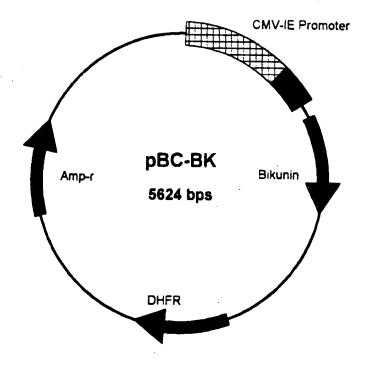


Figure 27

Figure 28(a): Short circuit current (Isc) trace to show the action of CHO rhBikunin (1-170) (10 ug/mL) on sodium dependent current in cultured cystic fibrosis human bronchial epithelial cells in vitro.

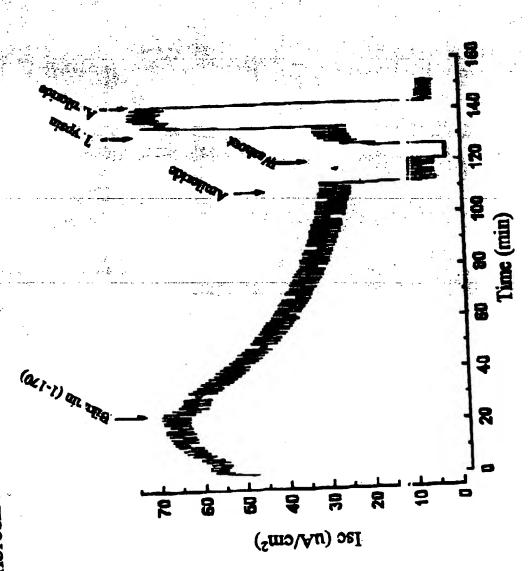
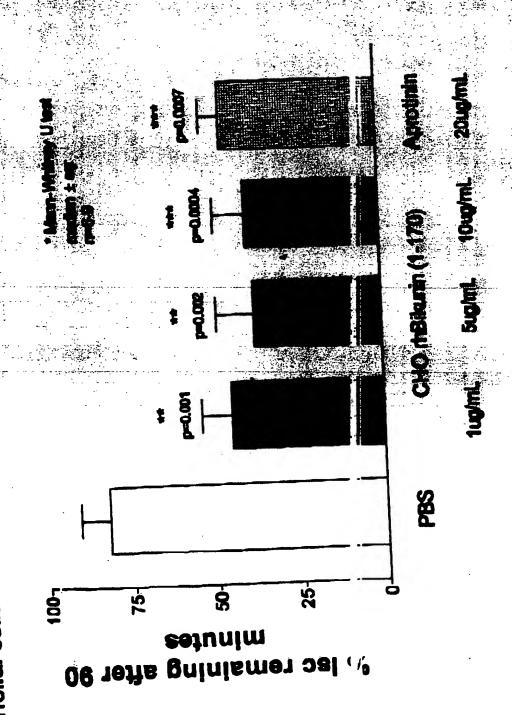


Figure 28(b): Percentage baseline short circuit current (les) remaining at 90 minutes after pretreatment with PBS, CHO mBilkum (FTZ) (10 ug/mL - 10 ug/mL) or Aprotinin (20 ug/mL) in cystic fibratis bronchial epithelial cells in vitro



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#### Flow Chart of CHO rhBikunin Purification Process Train

CHO TCF

SP-Sepharose, pH 5, Capture

UF/DF/Fil., pH 8.2, Concentration & Buffer Exchange

Q-Sepharose, pH 8.2, Capture, Dimer removal

Zn-IMAC, pH 7.2, Flowthrough, CHO protein removal

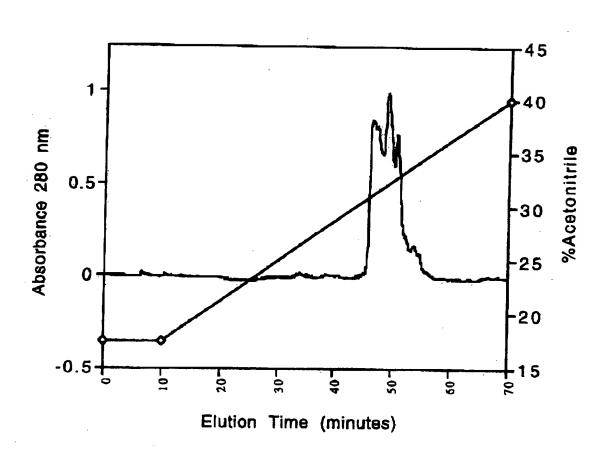
UF, pH 7.4, Concentration

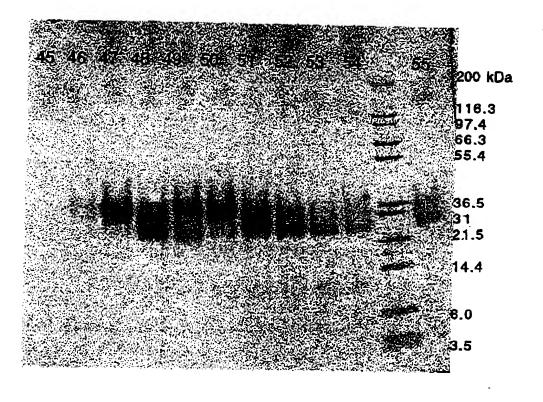
S-200, pH 7.2, Size Exclusion

ETOX Treatment, pH 7.2, Protective Pyrogen Removal

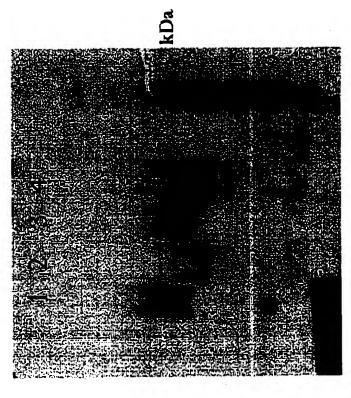
Figure 29

Figure & 30(a)





Deglycosylation of CHO-derived Bikunin



Lane 1: "High" MW bikunin prior to treatment

2: "High" MW bikunin post N-Glycosidase F
3: "Low" MW bikunin prior to treatment
4: "Low" MW bikunin post N-Glycosidase F